

S. aureus – Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop   | match           | match gene name   | % sim | % ident | length |
|--------|-----|--------|--------|-----------------|---|-------|---------|--------|
| ID     | ID  | (nt)   | (nt)   | accession       |   | (nt)  | (nt)    |        |
| 20     | 6   | 5089   | 4679   | gi 511839       | ORF1 [Staphylococcus bacteriophage phi 11]  | 100   | 100     | 411    |
| 149    | 3   | 2032   | 1577   | pir B49703 B497 | Int gene activator Rina - bacteriophage phi 11  | 100   | 100     | 456    |
| 149    | 5   | 2109   | 1912   | gi 166161       | Bacteriophage phi-11 int gene activator [Staphylococcus bacteriophage phi                   | 100   | 100     | 198    |
|        |     |        |        |                 |   |       |         |        |
| 349    | 2   | 558    | 409    | gi 166159       | Integrase (int) [Staphylococcus bacteriophage phi 11]                                       | 100   | 100     | 150    |
| 398    | 1   | 1372   | 707    | gi 166159       | Integrase (int) [Staphylococcus bacteriophage phi 11]                                       | 100   | 99      | 666    |
| 398    | 2   | 783    | 1001   | gi 455128       | Excisionase (xis) [Staphylococcus bacteriophage phi 11]                                     | 100   | 100     | 219    |
| 502    | 4   | 1914   | 1744   | gi 1204912      | H. influenzae predicted coding region HI0660 [Haemophilus influenzae]                       | 100   | 71      | 171    |
| 849    | 1   | 2      | 262    | gi 1373002      | Polyprotein [Bean common mosaic virus]  | 100   | 46      | 261    |
| 1349   | 1   | 277    | 140    | gi 143359       | Protein synthesis initiation factor 2 (infB) [Bacillus subtilis] gi 49319                   | 100   | 82      | 138    |
|        |     |        |        |                 | IF2 gene product [Bacillus subtilis]  |       |         |        |
| 2880   | 1   | 21     | 308    | gi 862933       | Protein kinase C inhibitor-I [Homo sapiens]   | 100   | 98      | 288    |
| 3085   | 1   | 428    | 216    | gi 1354211      | lPET112-like protein [Bacillus subtilis]  | 100   | 100     | 213    |
| 4168   | 2   | 571    | 398    | gi 1354211      | lPET112-like protein [Bacillus subtilis]  | 100   | 100     | 174    |
| 331    | 1   | 2      | 247    | gi 426473       | lNusG gene product [Staphylococcus carnosus]  | 98    | 95      | 246    |
| 207    | 2   | 1272   | 1463   | gi 460259       | Lenolase [Bacillus subtilis]  | 97    | 90      | 192    |
| 331    | 2   | 395    | 850    | gi 581638       | lL11 protein [Staphylococcus carnosus]  | 97    | 93      | 456    |
| 366    | 1   | 39     | 215    | gi 166161       | Bacteriophage phi-11 int gene activator [Staphylococcus bacteriophage phi                   | 97    | 95      | 177    |
|        |     |        |        |                 |   |       |         |        |
| 680    | 3   | 718    | 936    | gi 426473       | lNusG gene product [Staphylococcus carnosus]  | 97    | 97      | 219    |
| 3578   | 1   | 284    | 144    | gi 1339950      | Large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]                    | 97    | 79      | 141    |
| 157    | 1   | 321    | 518    | gi 1022726      | Unknown [Staphylococcus haemolyticus]   | 96    | 88      | 198    |
| 205    | 133 | 116470 | 116147 | gi 1165302      | lS10 [Bacillus subtilis]  | 96    | 91      | 324    |
|        |     |        |        |                 |   |       |         |        |
| 3919   | 1   | 48     | 401    | gi 871784       | lC1p-like ATP-dependent protease binding subunit [Bos taurus]                               | 96    | 81      | 354    |
| 4133   | 1   | 830    | 417    | gi 1022726      | Unknown [Staphylococcus haemolyticus]   | 96    | 84      | 414    |
| 4168   | 1   | 708    | 355    | gi 1354211      | lPET112-like protein [Bacillus subtilis]  | 96    | 95      | 354    |
| 4207   | 1   | 312    | 157    | gi 602031       | Similar to trimethylamine DH [Mycoplasma capricolum] piri 549950 S49950                     | 96    | 86      | 156    |
|        |     |        |        |                 | Probable trimethylamine dehydrogenase (EC 5.99.7) - Mycoplasma capricolum (SGC3) (fragment) |       |         |        |

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| 4227   | 2   | 152    | 331   | gi 871784       | Clp-like ATP-dependent protease binding subunit [Bos taurus]  | 96    | 81      | 180    |
| 4416   | 1   | 570    | 286   | gi 1022726      | Unknown [Staphylococcus haemolyticus]   | 96    | 84      | 285    |
| 22     | 1   | 858    | 430   | gi 511070       | UreG [Staphylococcus xylosus]   | 95    | 88      | 429    |
| 22     | 7   | 4362   | 4036  | gi 581787       | Urease gamma subunit [Staphylococcus xylosus]   | 95    | 79      | 327    |
| 82     | 6   | 8794   | 9114  | pir JG0008 JG00 | ribosomal protein S7 - Bacillus stearothermophilus  | 95    | 83      | 321    |
| 154    | 9   | 9280   | 7838  | gi 1354211      | PET112-like protein [Bacillus subtilis]   | 95    | 92      | 1443   |
| 186    | 3   | 2798   | 2055  | gi 1514656      | Serine O-acetyltransferase [Staphylococcus xylosus]   | 95    | 87      | 744    |
| 205    | 5   | 4406   | 4014  | gi 142462       | ribosomal protein S11 [Bacillus subtilis]   | 95    | 85      | 393    |
| 205    | 7   | 5017   | 4793  | gi 142459       | Initiation factor 1 [Bacillus subtilis]   | 95    | 84      | 225    |
| 205    | 21  | 11365  | 10991 | gi 1044974      | ribosomal protein L14 [Bacillus subtilis]   | 95    | 93      | 375    |
| 259    | 5   | 7288   | 6644  | sp P47995 YSEA_ | HYPOTHETICAL PROTEIN IN SECA 5' REGION (ORF1) (FRAGMENT).   | 95    | 85      | 645    |
| 302    | 3   | 1795   | 1097  | gi 40186        | Homologous to E. coli ribosomal protein L27 [Bacillus subtilis] gi 143592 L27   | 95    | 89      | 303    |
|        |     |        |       |                 | ribosomal protein [Bacillus subtilis] ir C21895 C21895 ribosomal protein L27 - Bacillus subtilis p P05657 RL27_BACSU_50S RIBOSOMAL PROTEIN L27 (BL30) (BL24) . ii 40175 L24 gene prod |       |         |        |
| 310    | 1   | 1579   | 1523  | gi 1177684      | Chorismate mutase [Staphylococcus xylosus]  | 95    | 92      | 945    |
| 414    | 1   | 2      | 163   | pir C48396 C483 | ribosomal protein L34 - Bacillus stearothermophilus   | 95    | 90      | 162    |
| 4185   | 2   | 125    | 277   | gi 1276841      | Glutamate synthase (GOGAT) [Porphyra purpurea]  | 95    | 86      | 153    |
| 22     | 2   | 1028   | 723   | gi 511069       | UreF [Staphylococcus xylosus]   | 94    | 91      | 306    |
| 22     | 5   | 5046   | 3310  | gi 410516       | Urease alpha subunit [Staphylococcus xylosus]   | 94    | 85      | 1737   |
| 60     | 4   | 815    | 1372  | gi 666116       | Glucose kinase [Staphylococcus xylosus]   | 94    | 87      | 558    |
| 205    | 118 | 110012 | 9536  | gi 1044978      | ribosomal protein S8 [Bacillus subtilis]  | 94    | 78      | 477    |
| 326    | 4   | 3378   | 2542  | gi 557492       | Dihydroxynaphthoic acid (DNA) synthetase [Bacillus subtilis] gi 143186  | 94    | 85      | 837    |
|        |     |        |       |                 | Dihydroxynaphthoic acid (DNA) synthetase [Bacillus subtilis]  |       |         |        |
| 414    | 3   | 737    | 955   | gi 467386       | Thiophen and furan oxidation [Bacillus subtilis]  | 94    | 77      | 219    |
| 426    | 3   | 2260   | 1823  | gi 1263908      | Putative [Staphylococcus epidermidis]   | 94    | 87      | 438    |
| 534    | 1   | 2      | 355   | gi 633650       | Enzyme II(mannitol) [Staphylococcus carnosus]   | 94    | 84      | 354    |
| 1017   | 1   | 1      | 229   | gi 149435       | Putative (Lactococcus lactis)   | 94    | 73      | 228    |
| 3098   | 1   | 330    | 184   | gi 413952       | Lipa-28d gene product [Bacillus subtilis]   | 94    | 50      | 147    |

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| 3232   | 1   | 630    | 316    | gi 1022725      | unknown [Staphylococcus haemolyticus]   | 94    | 84      | 315    |
| 42     | 5   | 2089   | 2259   | pir B18396 B483 | ribosomal protein L33 - <i>Bacillus stearothermophilus</i>  | 93    | 81      | 171    |
| 101    | 2   | 1745   | 1383   | gi 155345       | arsenic efflux pump protein [Plasmid pSX267]  | 93    | 82      | 363    |
| 205    | 124 | 112227 | 11865  | sp P14577 RL16_ | 50S RIBOSOMAL PROTEIN L16.  | 93    | 83      | 363    |
| 259    | 4   | 8291   | 5673   | gi 499335       | lsecA protein [Staphylococcus carnosus]   | 93    | 85      | 2619   |
| 275    | 1   | 2226   | 1114   | gi 633650       | enzyme II (mannitol) [Staphylococcus carnosus]  | 93    | 86      | 1113   |
| 444    | 6   | 6207   | 5773   | gi 1022726      | unknown [Staphylococcus haemolyticus]   | 93    | 81      | 435    |
| 491    | 1   | 152    | 622    | gi 46912        | ribosomal protein L13 [Staphylococcus carnosus]   | 93    | 88      | 471    |
| 607    | 6   | 1674   | 2033   | gi 1022726      | unknown [Staphylococcus haemolyticus]   | 93    | 83      | 360    |
| 653    | 1   | 973    | 488    | gi 580890       | translation initiation factor IF3 (AA 1-172) [Bacillus tearothermophilus]   | 93    | 77      | 486    |
| 1864   | 1   | 3      | 194    | gi 306553       | ribosomal protein small subunit [Homo sapiens]  | 93    | 93      | 192    |
| 2997   | 1   | 28     | 300    | gi 143390       | carbamyl phosphate synthetase [Bacillus subtilis]   | 93    | 82      | 273    |
| 3232   | 2   | 907    | 596    | gi 1022725      | unknown [Staphylococcus haemolyticus]   | 93    | 84      | 312    |
| 3761   | 2   | 794    | 621    | gi 1022725      | unknown [Staphylococcus haemolyticus]   | 93    | 88      | 174    |
| 16     | 1   | 3      | 374    | gi 142781       | putative cytoplasmic protein; putative [Bacillus subtilis] sp P37954 UVRB_BACSU_EXCINUCLEASE ABC SUBUNIT B (DINA PROTEIN) FRAGMENT. | 92    | 83      | 372    |
| 31     | 7   | 5915   | 6124   | gi 1136430      | IKIAA0185 protein [Homo sapiens]  | 92    | 46      | 210    |
| 56     | 19  | 126483 | 127391 | gi 467401       | unknown [Bacillus subtilis]   | 92    | 80      | 909    |
| 69     | 6   | 5882   | 6130   | gi 530200       | trophoblastin [Ovis aries]  | 92    | 53      | 249    |
| 171    | 3   | 2760   | 2362   | gi 517475       | D-amino acid transaminase [Staphylococcus haemolyticus]   | 92    | 86      | 399    |
| 205    | 112 | 7495   | 6962   | gi 49189        | lsecY gene product [Staphylococcus carnosus]  | 92    | 85      | 534    |
| 205    | 119 | 10812  | 110255 | gi 1044976      | ribosomal protein L5 [Bacillus subtilis]  | 92    | 82      | 558    |
| 219    | 1   | 710    | 357    | gi 1303812      | YqeV [Bacillus subtilis]  | 92    | 88      | 354    |
| 344    | 3   | 1575   | 1805   | gi 1405474      | CspC protein [Bacillus cereus]  | 92    | 85      | 231    |
| 699    | 1   | 20     | 361    | gi 413999       | lipa-75d gene product [Bacillus subtilis]   | 92    | 81      | 342    |
| 1343   | 1   | 2      | 160    | pir A45434 A454 | ribosomal protein L19 - <i>Bacillus stearothermophilus</i>  | 92    | 84      | 159    |

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|--------|------|-----|--------|--------|---------------|-----------|--|-------|---------|----------------|
| 1      | 1958 | 1   | 524    | 264    | lgi 407908    |           | lEliscr [Staphylococcus xylosus]   | 1     | 92      | 80             |
| 1      | 3578 | 2   | 718    | 386    | lgi 1339950   |           | large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]     | 1     | 92      | 78             |
| 1      | 3585 | 1   | 644    | 324    | lgi 1339950   |           | large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]     | 1     | 92      | 81             |
| 1      | 3640 | 1   | 4      | 402    | lgi 1022726   |           | lunknown [Staphylococcus haemolyticus]                                       | 1     | 92      | 81             |
| 1      | 4362 | 1   | 14     | 178    | lgi 450688    |           | lhsdM gene of EcoprrI gene product [Escherichia coli] pir S38437 S38437 hsdM | 92    | 78      | 165            |
| 1      | 4446 | 1   | 358    | 182    | lgi 1022725   |           | lprotein - Escherichia coli pir S09629 S09629 hypothetical protein A -       | 1     | 92      | 82             |
| 1      | 4549 | 1   | 462    | 232    | lgi 1022726   |           | lunknown [Staphylococcus haemolyticus]                                       | 1     | 92      | 80             |
| 1      | 4626 | 1   | 3      | 224    | lgi 1022725   |           | lunknown [Staphylococcus haemolyticus]                                       | 1     | 92      | 84             |
| 1      | 2    | 4   | 3980   | 4531   | lgi 535349    |           | lCodW [Bacillus subtilis]  | 1     | 91      | 74             |
| 1      | 28   | 1   | 2      | 1126   | lgi 1001376   |           | lhypothetical protein [Synechocystis sp.]                                    | 1     | 91      | 78             |
| 1      | 60   | 5   | 1354   | 1701   | lgi 1226043   |           | lorf2 downstream of glucose kinase [Staphylococcus xylosus]                  | 1     | 91      | 80             |
| 1      | 101  | 1   | 1989   | 1036   | lgi 1150728   |           | larsenic efflux pump protein [Plasmid pI258]                                 | 1     | 91      | 80             |
| 1      | 187  | 2   | 412    | 1194   | lgi 142559    |           | lATP synthase alpha subunit [Bacillus megaterium]                            | 1     | 91      | 79             |
| 1      | 205  | 122 | 111579 | 111298 | lgi 40149     |           | lS17 protein (AA 1-87) [Bacillus subtilis]                                   | 1     | 91      | 83             |
| 1      | 206  | 1   | 7      | 8184   | lgi 10262     |           | lglcA gene product [Staphylococcus carnosus]                                 | 1     | 91      | 83             |
| 1      | 306  | 1   | 2      | 3885   | lgi 1072418   |           | lglcA gene product [Staphylococcus carnosus]                                 | 1     | 91      | 83             |
| 1      | 306  | 1   | 3      | 5319   | lgi 143012    |           | lGMP synthetase [Bacillus subtilis]  | 1     | 91      | 78             |
| 1      | 310  | 1   | 3      | 2194   | lgi 1177685   |           | lIMP dehydrogenase [Bacillus subtilis]                                       | 1     | 91      | 79             |
| 1      | 343  | 4   | 1      | 2974   | lgi 949974    |           | lccPA gene product [Staphylococcus xylosus]                                  | 1     | 91      | 81             |
| 1      | 480  | 3   | 1      | 1606   | lgi 433991    |           | lATP synthase subunit beta [Bacillus subtilis]                               | 1     | 91      | 85             |
| 1      | 536  | 3   | 2026   | 1280   | lgi 143366    |           | ladenylosuccinate lyase (PUR-B) [Bacillus subtilis] Pir C29326 WZESDS        | 1     | 91      | 79             |
| 1      | 552  | 1   | 1      | 1064   | lgi 297874    |           | ladenylosuccinate lyase (EC 4.3.2.2) - Bacillus subtilis                     | 1     | 91      | 1437           |
| 1      | 637  | 1   | 1      | 1      | lgi 143597    |           | lfructose-bisphosphate aldolase [Staphylococcus carnosus] pir A19943 A49943  | 91    | 79      | 450            |
| 1      | 859  | 1   | 1      | 21     | lgi 386178    |           | lfructose-bisphosphate aldolase (EC 4.1.2.13) - taphylococcus carnosus       | 1     | 91      | 79             |
| 1      |      |     |        |        |               |           | (strain TM300)   | 1     | 91      | 1536           |
| 1      |      |     |        |        |               |           | lCTP synthetase [Bacillus subtilis]  | 1     | 91      | 66             |
| 1      |      |     |        |        |               |           | lunknown [Bacillus subtilis]   | 1     | 91      | 339            |

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| 1327   | 1   | 339    | 530    | gi 495558       | orfX [Bacillus subtilis]  | 91                                | 71      | 192    |      |
| 2515   | 1   | 466    | 275    | gi 51070        | UreG [Staphylococcus xylosus]   | 91                                | 85      | 192    |      |
| 2594   | 1   | 2      | 202    | gi 146824       | beta-cystathionase [Escherichia coli]                                       | 91                                | 75      | 201    |      |
| 3764   | 1   | 847    | 425    | gi 1022225      | unknown [Staphylococcus haemolyticus]                                       | 91                                | 78      | 423    |      |
| 4011   | 1   | 127    | 495    | gi 1022726      | unknown [Staphylococcus haemolyticus]                                       | 91                                | 79      | 369    |      |
| 4227   | 1   | 1      | 177    | gi 1296464      | ATPase [Lactococcus lactis]   | 91                                | 66      | 177    |      |
| 42     | 3   | 815    | 1033   | gi 520401       | catalase [Haemophilus influenzae]   | 90                                | 86      | 219    |      |
| 51     | 8   | 3717   | 4607   | gi 589899       | OppF gene product [Bacillus subtilis]                                       | 90                                | 74      | 891    |      |
| 129    | 3   | 5317   | 4001   | gi 1146206      | lglutamate dehydrogenase [Bacillus subtilis]                                | 90                                | 76      | 1317   |      |
| 164    | 117 | 116628 | 116933 | sp P03766 RS15  | 30S RIBOSOMAL PROTEIN S15 (BS18).   | 90                                | 74      | 306    |      |
| 171    | 5   | 2983   | 2819   | gi 517475       | D-amino acid transaminase [Staphylococcus haemolyticus]                     | 90                                | 78      | 165    |      |
| 205    | 4   | 4497   | 3550   | gi 142463       | RNA polymerase alpha-core-subunit [Bacillus subtilis]                       | 90                                | 76      | 948    |      |
| 205    | 6   | 4748   | 4410   | gi 104989       | ribosomal protein S13 [Bacillus subtilis]                                   | 90                                | 73      | 339    |      |
| 205    | 110 | 7165   | 6404   | gi 49789        | lsecY gene product [Staphylococcus carnosus]                                | 90                                | 81      | 762    |      |
| 205    | 111 | 6645   | 6472   | gi 49189        | lsecY gene product [Staphylococcus carnosus]                                | 90                                | 78      | 174    |      |
| 205    | 127 | 113692 | 113345 | gi 786157       | Ribosomal Protein S19 [Bacillus subtilis]                                   | 90                                | 79      | 348    |      |
| 205    | 131 | 115838 | 115496 | gi 1165303      | L3 [Bacillus subtilis]  | 90                                | 79      | 363    |      |
| 260    | 1   | 5      | 7023   | 5773            | gi 1161380  | IcaA [Staphylococcus epidermidis] | 90      | 78     | 1251 |
| 299    | 6   | 3378   | 3947   | gi 467440       | 'phosphoribosylpyrophosphate synthetase [Bacillus subtilis] gi 40218 PRPP   | 90                                | 78      | 570    |      |
|        | 1   | 1      | 1      | 1               | synthetase (AA 1-317) [Bacillus subtilis]                                   | 90                                | 80      | 189    |      |
| 320    | 2   | 1025   | 1717   | gi 312143       | carbamoyl-phosphate synthase (glutamine-hydrolysing) [Bacillus aldotyticus] | 90                                | 75      | 693    |      |
| 330    | 4   | 1581   | 1769   | gi 986963       | lbeta-tubulin [Sporidiobolus pararoseus]                                    | 90                                | 77      | 432    |      |
| 369    | 1   | 954    | 523    | pir S34762 S347 | L-serine dehydratase beta chain - Clostridium sp.                           | 90                                | 80      | 186    |      |
| 557    | 1   | 1      | 3      | gi 151589       | M. jannaschii predicted coding region MJ1624 [Methanococcus jannaschii]     | 90                                | 54      | 534    |      |
| 663    | 2   | 667    | 1200   | gi 143786       | tryptophanyl-tRNA synthetase (EC 6.1.1.2) [Bacillus subtilis]               | 90                                | 73      | 534    |      |
|        | 1   | 1      | 1      | 1               | pir U0481 YWB5 tryptophan-tRNA ligase (EC 6.1.1.2) - Bacillus subtilis      | 90                                | 81      | 195    |      |
| 717    | 1   | 1      | 261    | gi 143065       | lhubst [Bacillus stearothermophilus]  | 90                                | 79      | 261    |      |
| 745    | 4   | 1059   | 865    | gi 1205433      | H. influenzae predicted coding region HI1190 [Haemophilus influenzae]       | 90                                | 81      | 195    |      |

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| 1007   | 1   | 386    | 565   | gi 143366       | adenylosuccinate lyase (PUR-B) [Bacillus subtilis] pir C29326 WZBDS   | 90    | 77      | 180    |
|        |     |        |       |                 | adenylosuccinate lyase (EC 4.3.2.2) - Bacillus subtilis   |       |         |        |
| 1054   | 1   | 579    | 331   | gi 1033122      | ORF_f729 [Escherichia coli]   | 90    | 50      | 249    |
| 1156   | 1   | 117    | 707   | gi 1477776      | C1pp [Bacillus subtilis]  | 90    | 80      | 591    |
| 1180   | 1   | 408    | 205   | gi 1377831      | unknown [Bacillus subtilis]   | 90    | 74      | 204    |
| 1253   | 1   | 1      | 462   | gi 40046        | phosphoglucose isomerase A (AA 1-449) [Bacillus stearothermophilus]<br>ir S15936 NUBSSA glucose-6-phosphate isomerase (EC 5.3.1.9) A - cillus | 90    | 75      | 462    |
|        |     |        |       |                 | stearothermophilus  |       |         |        |
| 2951   | 1   | 3      | 269   | gi 144816       | formyltetrahydrofolate synthetase (FTHFS) (ttg start codon) (EC .3.4.3)   | 90    | 76      | 267    |
|        |     |        |       |                 | [Moorella thermoacetica]  |       |         |        |
| 3140   | 1   | 327    | 166   | gi 1070014      | protein-dependent [Bacillus subtilis]   | 90    | 52      | 162    |
| 4594   | 1   | 3      | 233   | gi 871784       | C1p-like ATP-dependent protease binding subunit [Bos taurus]  | 90    | 76      | 231    |
| 87     | 1   | 1028   | 1750  | gi 467327       | unknown [Bacillus subtilis]   | 89    | 75      | 723    |
| 112    | 1   | 2      | 505   | gi 153741       | ATP-binding protein [Streptococcus mutans]  | 89    | 77      | 504    |
| 118    | 1   | 120    | 398   | gi 1303804      | YqeQ [Bacillus subtilis]  | 89    | 75      | 279    |
| 128    | 4   | 3545   | 3757  | gi 460257       | triose phosphate isomerase [Bacillus subtilis]  | 89    | 84      | 213    |
| 164    | 12  | 11667  | 12755 | gi 39954        | lIF2 (aa 1-741) [Bacillus stearothermophilus]   | 89    | 80      | 1089   |
| 205    | 13  | 7875   | 7405  | gi 216338       | ORF for L15 ribosomal protein [Bacillus subtilis]   | 89    | 76      | 471    |
| 205    | 132 | 116152 | 15823 | gi 1163303      | L3 [Bacillus subtilis]  | 89    | 80      | 330    |
| 270    | 3   | 2407   | 2207  | pir C41902 C419 | arsenate reductase (EC 1.1.1.1) - Staphylococcus xylosus plasmid pSX267   | 89    | 81      | 201    |
| 395    | 2   | 157    | 672   | gi 520574       | glutamate racemase [Staphylococcus haemolyticus]  | 89    | 80      | 516    |
| 494    | 1   | 3      | 839   | gi 396259       | protease [Staphylococcus epidermidis]   | 89    | 77      | 837    |
| 510    | 1   | 1      | 444   | gi 40046        | phosphoglucose isomerase A (AA 1-449) [Bacillus stearothermophilus]<br>ir S15936 NUBSSA glucose-6-phosphate isomerase (EC 5.3.1.9) A - cillus | 89    | 74      | 444    |
|        |     |        |       |                 | stearothermophilus  |       |         |        |
| 615    | 1   | 2124   | 1210  | gi 1303812      | YqeV [Bacillus subtilis]  | 89    | 74      | 915    |
| 841    | 1   | 18     | 341   | gi 1165303      | L3 [Bacillus subtilis]  | 89    | 80      | 324    |
|        |     |        |       |                 |   |       |         |        |
| 1111   | 1   | 352    | 813   | gi 47146        | thermonuclease [Staphylococcus intermedius]   | 89    | 70      | 462    |
| 1875   | 1   | 2      | 256   | gi 1205108      | ATP-dependent protease binding subunit [Haemophilus influenzae]   | 89    | 82      | 255    |
| 2963   | 1   | 11     | 367   | gi 467458       | cell division protein [Bacillus subtilis]   | 89    | 83      | 357    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start   | Stop    | match           | match gene name  | % sim | % ident | length |
|--------|-----|---------|---------|-----------------|--|-------|---------|--------|
| ID     | ID  | (nt)    | (nt)    | accession       |  |       |         | (nt)   |
| 3020   | 1   | 90      | 1 362   | gi 1239988      | hypothetical protein [Bacillus subtilis]                                 | 1     | 89      | 66     |
| 3565   | 1   | 1 2     | 1 400   | gi 1256635      | dihydroxy-acid dehydratase [Bacillus subtilis]                           | 1     | 89      | 75     |
| 3586   | 1   | 1 105   | 1 314   | gi 580832       | ATP synthase subunit gamma [Bacillus subtilis]                           | 1     | 89      | 82     |
| 3629   | 1   | 1 794   | 1 399   | gi 1009366      | Respiratory nitrate reductase [Bacillus subtilis]                        | 1     | 89      | 78     |
| 3688   | 1   | 1 2     | 1 400   | gi 1146206      | lglutamate dehydrogenase [Bacillus subtilis]                             | 1     | 89      | 75     |
| 3699   | 1   | 1 794   | 1 399   | gi 1339950      | large subunit of NADH-dependent glutamate synthase [Plectonema boryanum] | 1     | 89      | 75     |
| 4016   | 1   | 1 428   | 1 216   | gi 1009366      | Respiratory nitrate reductase [Bacillus subtilis]                        | 1     | 89      | 71     |
| 4177   | 1   | 1 471   | 1 301   | gi 149426       | putative [Lactococcus lactis]  | 1     | 89      | 76     |
| 4436   | 1   | 1 601   | 1 302   | gi 1022725      | lunkown [Staphylococcus haemolyticus]                                    | 1     | 89      | 80     |
| 4635   | 1   | 1 320   | 1 162   | gi 1022725      | lunkown [Staphylococcus haemolyticus]                                    | 1     | 89      | 73     |
| 2      | 2   | 1 1330  | 1 2676  | gi 520754       | putative [Bacillus subtilis]   | 1     | 88      | 76     |
| 42     | 2   | 1 468   | 1 848   | sp P42321 CATAL | CATALASE (EC 1.11.1.6).  | 1     | 88      | 76     |
| 53     | 5   | 1 6389  | 1 4722  | gi 474177       | alpha-D-1,4-glucosidase [Staphylococcus xylosus]                         | 1     | 88      | 80     |
| 56     | 116 | 1 18018 | 1 18617 | gi 467411       | recombination protein [Bacillus subtilis]                                | 1     | 88      | 77     |
| 60     | 3   | 1 376   | 1 843   | gi 666116       | glucose kinase [Staphylococcus xylosus]                                  | 1     | 88      | 77     |
| 70     | 2   | 1 1583  | 1 1245  | gi 44095        | replication initiator protein [Listeria monocytogenes]                   | 1     | 88      | 74     |
| 82     | 8   | 1 11514 | 1 12719 | pir A60663 A606 | translation elongation factor Tu - Bacillus subtilis                     | 1     | 88      | 79     |
| 103    | 7   | 1 4179  | 1 4391  | gi 167181       | serine/threonine kinase receptor [Brassica napus]                        | 1     | 88      | 77     |
| 114    | 8   | 1 7732  | 1 8232  | gi 1022726      | lunkown [Staphylococcus haemolyticus]                                    | 1     | 88      | 72     |
| 118    | 2   | 1 308   | 1 2011  | gi 1303804      | YqeQ [Bacillus subtilis]   | 1     | 88      | 77     |
| 141    | 3   | 1 657   | 1 1136  | gi 1405446      | transketolase [Bacillus subtilis]  | 1     | 88      | 72     |
| 148    | 7   | 1 5871  | 1 6116  | gi 1118002      | dihydropteroate synthase [Staphylococcus haemolyticus]                   | 1     | 88      | 78     |
| 165    | 3   | 1 1428  | 1 2231  | gi 40053        | phenylalanyl-tRNA synthetase alpha subunit [Bacillus subtilis]           | 1     | 88      | 80     |
|        |     |         |         |                 | ir S11730 YFB5A phenylalanine-tRNA ligase (EC 6.1.1.20) alpha ain -      | 1     |         |        |
|        |     |         |         |                 | Bacillus subtilis  | 1     |         |        |
| 205    | 128 | 1 15027 | 1 14185 | gi 1165306      | L2 [Bacillus subtilis]   | 1     | 88      | 82     |
| 225    | 1   | 1 1569  | 1 898   | gi 1303840      | Yqfs [Bacillus subtilis]   | 1     | 88      | 78     |
| 235    | 1   | 1 2     | 1 1975  | gi 452309       | lvalyl-tRNA synthetase [Bacillus subtilis]                               | 1     | 88      | 76     |

| Contig | lORE | Start | Stop | match            | match gene name   | % sim | % ident | length |
|--------|------|-------|------|------------------|---|-------|---------|--------|
| ID     | ID   | (nt)  | (nt) | accession        |   | (nt)  |         | (nt)   |
| 339    | 3    | 2060  | 1566 | lgi 1118002      | ldihydropteroate synthase [Staphylococcus haemolyticus]   | 88    | 73      | 495    |
| 443    | 4    | 4325  | 2928 | lgi 5585559      | pyrimidine nucleoside phosphorylase [Bacillus subtilis]   | 88    | 73      | 1398   |
| 532    | 1    | 3     | 419  | lgi 143797       | lvalyl-tRNA synthetase [Bacillus stearothermophilus] sp P11931 SYV_BACST  | 88    | 78      | 417    |
| 534    | 3    | 2504  | 2968 | lgi 153049       | mannitol-specific enzyme-III (Staphylococcus carnosus) pir JQ0088 JQ0088  | 88    | 82      | 465    |
|        |      |       |      |                  | phosphotransferase system enzyme II (EC 7.1.69), mannitol-specific, factor III - Staphylococcus carnosus sp P17876 PTMA_STACA PTS SYSTEM, MANNITOL-SPECIFIC IIIA COMPONENT IIIA-MTL ( |       |         |        |
| 705    | 2    | 584   | 399  | lgi 710018       | nitrite reductase (nirB) [Bacillus subtilis]  | 88    | 70      | 186    |
| 1000   | 2    | 1824  | 1309 | lgi 1022726      | unknown [Staphylococcus haemolyticus]   | 88    | 78      | 516    |
| 1299   | 1    | 587   | 324  | lgi 401786       | phosphomannomutase [Mycoplasma pirum]   | 88    | 55      | 264    |
| 1341   | 2    | 170   | 400  | lgi 39963        | ribosomal protein L20 (AA 1-119) [Bacillus stearothermophilus] ir S05348 R5BS20 ribosomal protein L20 - Bacillus eartohermophilus   | 88    | 82      | 231    |
| 1386   | 1    | 41    | 214  | lpir B47154 B471 | signal recognition particle 54K chain homolog Ffh - Bacillus subtilis   | 88    | 71      | 174    |
| 1386   | 2    | 183   | 533  | lpir B47154 B471 | signal recognition particle 54K chain homolog Ffh - Bacillus subtilis   | 88    | 73      | 351    |
| 2949   | 1    | 704   | 399  | lgi 535350       | lCodX [Bacillus subtilis]   | 88    | 73      | 306    |
| 2984   | 1    | 5     | 169  | lgi 218277       | lO-acetylserine (thiol) lyase [Spinacia oleracea]   | 88    | 70      | 165    |
| 3035   | 1    | 1     | 138  | lgi 493083       | lhydroxyacetone kinase [Citrobacter freundii]   | 88    | 67      | 138    |
| 3089   | 1    | 3     | 152  | lgi 606055       | lORF_f746 [Escherichia coli]  | 88    | 88      | 150    |
| 3917   | 1    | 817   | 410  | lgi 143378       | lpyruvate decarboxylase (E-1) beta subunit [Bacillus subtilis] gi 1377836   | 88    | 77      | 408    |
|        |      |       |      |                  | lpyruvate decarboxylase E-1 beta subunit [Bacillus subtilis]  |       |         |        |
| 4199   | 1    | 680   | 342  | lgi 1405454      | laconitase [Bacillus subtilis]  | 88    | 82      | 339    |
| 4201   | 1    | 734   | 369  | lgi 515938       | lglutamate synthase (ferredoxin) [Synechocystis sp.] pir S46957 S46957  | 88    | 84      | 366    |
|        |      |       |      |                  | lglutamate synthase (ferredoxin) (EC 1.4.7.1) - ynechocystis sp.  |       |         |        |
| 4274   | 1    | 1     | 336  | lgi 515938       | lglutamate synthase (ferredoxin) [Synechocystis sp.] pir S46957 S46957  | 88    | 84      | 336    |
|        |      |       |      |                  | lglutamate synthase (ferredoxin) (EC 1.4.7.1) - ynechocystis sp.  |       |         |        |
| 4308   | 1    | 794   | 399  | lgi 1146206      | lglutamate dehydrogenase [Bacillus subtilis]  | 88    | 71      | 396    |
| 2      | 5    | 4570  | 6000 | lgi 535350       | lCodX [Bacillus subtilis]   | 87    | 70      | 1431   |
| 52     | 8    | 6781  | 6482 | lgi 1064791      | lfunction unknown [Bacillus subtilis]   | 87    | 66      | 300    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop   | match            | gene name   | % sim | % ident | length |
|--------|-----|--------|--------|------------------|---|-------|---------|--------|
| ID     | ID  | (nt)   | (nt)   | accession        |   | (nt)  |         | (nt)   |
| 73     | 3   | 1584   | 2480   | gi 142992        | glycerol kinase (glpK) (EC 2.7.1.30) [Bacillus subtilis] pir B45868 B45868  | 87    | 72      | 897    |
|        |     |        |        |                  | glycerol kinase (EC 2.7.1.30) - Bacillus subtilis sp P18157 GLPK_BACSU      |       |         |        |
|        |     |        |        |                  | GLYCEROL KINASE (EC 2.7.1.30) (ATP:GLYCEROL -PHOSPHOTRANSFERASE)            |       |         |        |
|        |     |        |        |                  | (GLYCEROKINASE) (GK) .  |       |         |        |
| 98     | 112 | 8813   | 9100   | gi 467433        | unknown [Bacillus subtilis]   | 87    | 62      | 288    |
| 124    | 4   | 4265   | 2988   | gi 556886        | serine hydroxymethyltransferase [Bacillus subtilis] pir S49363 S49363       | 87    | 77      | 1278   |
|        |     |        |        |                  | serine hydroxymethyltransferase - Bacillus subtilis                         |       |         |        |
| 124    | 6   | 4457   | 4032   | gi 556883        | Unknown [Bacillus subtilis]   | 87    | 66      | 426    |
| 148    | 5   | 3741   | 4559   | gi 467460        | Unknown [Bacillus subtilis]   | 87    | 70      | 819    |
| 164    | 13  | 112710 | 113810 | gi 39954         | lif2 (aa 1-741) [Bacillus stearothermophilus]                               | 87    | 72      | 1101   |
| 177    | 2   | 1104   | 2126   | gi 467385        | Unknown [Bacillus subtilis]   | 87    | 78      | 1023   |
| 199    | 1   | 1982   | 1158   | gi 143527        | iron-sulfur protein [Bacillus subtilis]                                     | 87    | 77      | 825    |
| 199    | 2   | 4717   | 2933   | pir A27763 A277  | succinate dehydrogenase (EC 1.3.99.1) flavoprotein - Bacillus subtilis      | 87    | 80      | 1785   |
| 205    | 123 | 111782 | 11543  | gi 1044972       | ribosomal protein L29 [Bacillus subtilis]                                   | 87    | 78      | 240    |
| 205    | 125 | 113275 | 112607 | gi 1165309       | IS3 [Bacillus subtilis]   | 87    | 75      | 669    |
| 222    | 1   | 2033   | 11107  | gi 1177249       | lrec233 gene product [Bacillus subtilis]                                    | 87    | 70      | 927    |
| 236    | 3   | 1635   | 1333   | gi 1146198       | ferredoxin [Bacillus subtilis]  | 87    | 80      | 303    |
| 246    | 5   | 2585   | 12292  | gi 467373        | ribosomal protein S18 [Bacillus subtilis]                                   | 87    | 77      | 294    |
| 260    | 2   | 4189   | 3422   | gi 1161382       | lcaC [Staphylococcus epidermidis]   | 87    | 72      | 768    |
| 320    | 3   | 1696   | 2391   | gi 1312443       | carbamoyl-phosphate synthase (glutamine-hydrolysing) [Bacillus aldoliticus] | 87    | 80      | 696    |
| 380    | 4   | 1165   | 1383   | gi 142570        | ATP synthase c subunit [Bacillus firmus]                                    | 87    | 80      | 219    |
| 414    | 4   | 900    | 1073   | gi 467386        | thiophen and furan oxidation [Bacillus subtilis]                            | 87    | 77      | 174    |
| 425    | 2   | 1003   | 794    | gi 1046166       | lplin repressor [Mycoplasma genitalium]                                     | 87    | 69      | 210    |
| 448    | 1   | 1255   | 722    | gi 405134        | acetate kinase [Bacillus subtilis]  | 87    | 75      | 534    |
| 480    | 1   | 1      | 1      | gi 142559        | ATP synthase alpha subunit [Bacillus megaterium]                            | 87    | 79      | 711    |
| 481    | 1   | 2      | 352    | isp Q06797 RL1_B | 50S RIBOSOMAL PROTEIN L1 (BL1) .  | 87    | 72      | 351    |
| 677    | 2   | 359    | 955    | gi 460911        | fructose-bisphosphate aldolase [Bacillus subtilis]                          | 87    | 78      | 597    |
| 677    | 3   | 934    | 1284   | gi 460911        | fructose-bisphosphate aldolase [Bacillus subtilis]                          | 87    | 78      | 351    |
| 876    | 1   | 3      | 452    | gi 1146247       | asparaginyl-tRNA synthetase [Bacillus subtilis]                             | 87    | 79      | 450    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF  | Start | Stop   | match     | gene name   | % sim  | % ident | length |      |
|--------|------|-------|--------|-----------|-------------|--|---------|--------|------|
| ID     | ID   | (nt)  | (nt)   | accession |             | (nt)   | (nt)    |        |      |
| 1      | 1376 | 1     | 426    | 214       | gi 10655555 | EF46H6.4 gene product [Caenorhabditis elegans]   | 87      | 75     | 213  |
| 1      | 2206 | 1     | 1      | 3         | gi 215098   | lexcisionase [Bacteriophage 154a]  | 87      | 72     | 372  |
| 1      | 2938 | 1     | 1      | 3         | gi 508979   | GTP-binding protein [Bacillus subtilis]  | 87      | 69     | 288  |
| 1      | 3081 | 2     | 1      | 126       | gi 467399   | IMP dehydrogenase [Bacillus subtilis]  | 87      | 72     | 183  |
| 1      | 3535 | 1     | 1      | 3         | gi 1405454  | aconitase [Bacillus subtilis]  | 87      | 80     | 399  |
| 1      | 4238 | 1     | 1      | 547       | gi 603769   | HutU protein, urocanase [Bacillus subtilis]  | 87      | 73     | 273  |
| 1      | 4    | 8     | 10427  | 8736      | gi 603769   | HutU protein, urocanase [Bacillus subtilis]  | 86      | 72     | 1692 |
| 1      | 22   | 6     | 4190   | 3738      | gi 410515   | lurease beta subunit [Staphylococcus xylosus]  | 86      | 73     | 453  |
| 1      | 54   | 2     | 2480   | 1572      | gi 289287   | UDP-glucose pyrophosphorylase [Bacillus subtilis]  | 86      | 70     | 909  |
| 1      | 124  | 3     | 2336   | 1713      | gi 556887   | uracil phosphoribosyltransferase [Bacillus subtilis] pir S49364 S49364                           | 86      | 74     | 624  |
| 1      | 148  | 3     | 1349   | 3448      | gi 467458   | uracil phosphoribosyltransferase - Bacillus subtilis   | 86      | 75     | 2100 |
| 1      | 148  | 4     | 3638   | 3859      | gi 467460   | lcell division protein [Bacillus subtilis]   | 86      | 73     | 222  |
| 1      | 152  | 3     | 1340   | 2086      | gi 1377835  | lpyruvate decarboxylase E-1 alpha subunit [Bacillus subtilis]                                    | 86      | 75     | 747  |
| 1      | 164  | 118   | 117347 | 119467    | gi 1184680  | lpolynucleotide phosphorylase [Bacillus subtilis]  | 86      | 72     | 2121 |
| 1      | 180  | 2     | 554    | 1159      | gi 143467   | ribosomal protein S4 [Bacillus subtilis]   | 86      | 80     | 606  |
| 1      | 205  | 3     | 2966   | 2592      | gi 142464   | ribosomal protein L17 [Bacillus subtilis]  | 86      | 77     | 375  |
| 1      | 205  | 26    | 13364  | 12990     | gi 40107    | ribosomal protein L22 [Bacillus stearothermophilus] iri S10612 S10612                            | 86      | 75     | 375  |
| 1      | 246  | 7     | 3463   | 3140      | gi 467375   | ribosomal protein L22 - Bacillus stearothermophilus  | 86      | 70     | 324  |
| 1      | 299  | 3     | 1196   | 1540      | gi 39656    | lspovG gene product [Bacillus megaterium]  | 86      | 70     | 345  |
| 1      | 299  | 7     | 3884   | 4345      | gi 467440   | l'phosphoribosylpyrophosphate synthetase [Bacillus subtilis] gi 40218 PRPP                       | 86      | 78     | 462  |
| 1      | 304  | 5     | 2170   | 2523      | gi 666983   | lputative ATP binding subunit [Bacillus subtilis]  | 86      | 65     | 354  |
| 1      | 310  | 2     | 1487   | 1678      | gi 1177684  | lchorismate mutase [Staphylococcus xylosus]  | 86      | 71     | 192  |
| 1      | 337  | 5     | 2086   | 3405      | gi 487434   | lisocitrate dehydrogenase [Bacillus subtilis]  | 86      | 78     | 1320 |
| 1      | 339  | 2     | 1489   | 1109      | gi 1118003  | ldihydroneopterin aldolase [Staphylococcus haemolyticus]   | 86      | 77     | 381  |
| 1      | 358  | 2     | 2124   | 3440      | gi 1146219  | l28.2% of identity to the Escherichia coli GTP-binding protein Era; putative [Bacillus subtilis] | 86      | 73     | 1317 |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop   | match       | match gene name  | % sim | % ident | length |
|--------|-----|--------|--------|-------------|--|-------|---------|--------|
| ID     | ID  | (nt)   | (nt)   | accession   |  | (nt)  | (nt)    | (nt)   |
| 404    | 2   | 1015   | 2058   | gi 1303817  | YqFA [Bacillus subtilis]   | 86    | 78      | 1044   |
| 581    | 2   | 661    | 452    | gi 40056    | lphoP gene product [Bacillus subtilis]   | 86    | 71      | 210    |
| 642    | 2   | 338    | 1075   | gi 1176399  | lEpif [Staphylcoccus epidermidis]  | 86    | 72      | 738    |
| 770    | 1   | 622    | 347    | gi 1433328  | lphoP protein (put.); putative [Bacillus subtilis]   | 86    | 69      | 276    |
| 865    | 1   | 1777   | 890    | gi 1146247  | lasparginyl-tRNA synthetase [Bacillus subtilis]  | 86    | 74      | 888    |
| 868    | 2   | 963    | 1133   | gi 1002911  | transmembrane protein [Saccharomyces cerevisiae]   | 86    | 69      | 171    |
| 904    | 1   | 1      | 162    | gi 1303912  | YqhW [Bacillus subtilis]   | 86    | 72      | 162    |
| 989    | 1   | 35     | 433    | gi 1303993  | YqkL [Bacillus subtilis]   | 86    | 76      | 399    |
| 1212   | 1   | 296    | 150    | gi 414014   | lipa-90d gene product [Bacillus subtilis]  | 86    | 70      | 147    |
| 1323   | 1   | 2      | 148    | gi 40041    | lpyruvate dehydrogenase (lipoamide) [Bacillus stearothermophilus]<br>ir S10798 DEBSPF pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) pha chain<br>- Bacillus stearothermophilus | 86    | 75      | 147    |
| 3085   | 2   | 540    | 310    | gi 1354211  | lPET112-like protein [Bacillus subtilis]   | 86    | 86      | 231    |
| 3847   | 1   | 1      | 228    | gi 296464   | lATPase [Lactococcus lactis]   | 86    | 63      | 228    |
| 4487   | 1   | 476    | 240    | gi 1022726  | unknown [Staphylococcus haemolyticus]  | 86    | 73      | 237    |
| 4583   | 1   | 372    | 187    | gi 1022725  | unknown [Staphylococcus haemolyticus]  | 86    | 79      | 186    |
| 25     | 5   | 4287   | 5039   | gi 1502421  | l3-ketoacyl-acyl carrier protein reductase [Bacillus subtilis]   | 85    | 64      | 753    |
| 56     | 121 | 130627 | 129395 | gi 1408507  | lpyrimidine nucleoside transport protein [Bacillus subtilis]   | 85    | 69      | 1233   |
| 68     | 1   | 332    | 1192   | gi 467376   | lunknown [Bacillus subtilis]   | 85    | 74      | 861    |
| 73     | 2   | 880    | 1707   | gi 142992   | lglycerol kinase (glpK) (EC 2.7.1.30) [Bacillus subtilis] pir B45868 B45868  | 85    | 72      | 828    |
|        |     |        |        |             | lglycerol kinase (EC 2.7.1.30) - Bacillus subtilis sp P18157 GLPK_BACSU  |       |         |        |
|        |     |        |        |             | lGLYCEROL KINASE (EC 2.7.1.30) (ATP:GLYCEROL -PHOSPHOTRANSFERASE)<br>(GLYCEROKINASE) (GK).   |       |         |        |
| 106    | 4   | 1505   | 3490   | gi 143766   | lthrSv (EC 6.1.1.3) [Bacillus subtilis]  | 85    | 74      | 1986   |
| 128    | 2   | 1153   | 2202   | gi 311924   | lglyceraldehyde-3-phosphate dehydrogenase [Clostridium pasteurianum]<br>pir S34254 S34254 glyceraldehyde-3-phosphate dehydrogenase (EC .2.1.12) -<br>Clostridium pasteurianum    | 85    | 75      | 1050   |
| 129    | 4   | 6466   | 5252   | gi 1064807  | lORTHININE AMINOTRANSFERASE [Bacillus subtilis]  | 85    | 73      | 1215   |
| 138    | 6   | 3475   | 5673   | gi 11072419 | lglcB gene product [Staphylococcus carnosus]   | 85    | 74      | 2199   |
| 189    | 1   | 2      | 169    | gi 467385   | lunknown [Bacillus subtilis]   | 85    | 65      | 168    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | lORE | Start | Stop   | match     | match gene name  | % sim   | % ident | length |      |
|--------|------|-------|--------|-----------|------------------|---|---------|--------|------|
| ID     | ID   | (nt)  | (nt)   | accession |                  | (nt)  |         | (nt)   |      |
| 1      | 205  | 115   | 8624   | 8106      | gi 1044981       | ribosomal protein S5 [Bacillus subtilis]  | 85      | 75     | 519  |
|        | 205  | 120   | 110928 | 110596    | lpir A02819 R5BS | ribosomal protein L24 - Bacillus stearothermophilus   | 85      | 72     | 333  |
|        | 220  | 6     | 6490   | 6101      | gi 48980         | lsecA gene product [Bacillus subtilis]  | 85      | 66     | 390  |
|        | 231  | 4     | 4877   | 3159      | gi 1002520       | lMuts [Bacillus subtilis]   | 85      | 70     | 1719 |
|        | 243  | 9     | 8013   | 8783      | gi 414011        | lipa-87r gene product [Bacillus subtilis]   | 85      | 72     | 771  |
|        | 249  | 2     | 5894   | 3186      | gi 1405454       | aconitase [Bacillus subtilis]   | 85      | 73     | 2709 |
|        | 302  | 1     | 140    | 475       | gi 40173         | homolog of E. coli ribosomal protein L21 [Bacillus subtilis]<br>ir S18439 S18439 Ribosomal protein L21 - Bacillus subtilis<br>  p P26908 RL21_BACSU_50S_RIBOSOMAL_PROTEIN_L21_(BL20). | 85      | 72     | 336  |
|        | 333  | 1     | 5445   | 2968      | gi 442360        | ClpC adenosine triphosphatase [Bacillus subtilis]   | 85      | 69     | 2478 |
|        | 364  | 6     | 6082   | 8196      | gi 871784        | Clp-like ATP-dependent protease binding subunit [Bos taurus]  | 85      | 68     | 2115 |
|        | 448  | 2     | 1992   | 1339      | gi 405134        | acetate kinase [Bacillus subtilis]  | 85      | 68     | 654  |
|        | 747  | 1     | 1251   | 853       | gi 1373157       | orf-X; hypothetical protein; Method: conceptual translation supplied by<br>  author [Bacillus subtilis]   | 85      | 73     | 399  |
|        | 886  | 2     | 159    | 467       | gi 541768        | hemin permease [Yersinia enterocolitica]  | 85      | 55     | 309  |
|        | 1089 | 1     | 1208   | 606       | lpir B47154 B471 | signal recognition particle 54K chain homolog Ffh - Bacillus subtilis   | 85      | 71     | 603  |
|        | 1163 | 1     | 816    | 409       | gi 304155        | diaminopimelate decarboxylase [Bacillus methanolicus] sp P41023 DCDA_BACMT<br>  DIAMINOPIMELATE DECARBOXYLASE (EC 4.1.1.20) DAP DECARBOXYLASE.  | 85      | 62     | 408  |
|        | 1924 | 1     | 487    | 251       | gi 215098        | excisionase [Bacteriophage 154a]  | 85      | 73     | 237  |
|        | 2932 | 1     | 776    | 390       | gi 11041099      | Pyruvate Kinase [Bacillus licheniformis]  | 85      | 71     | 387  |
|        | 3030 | 1     | 3      | 275       | gi 42370         | pyruvate formate-lyase (AA 1-760) [Escherichia coli] ir S01788 S01788<br>  formate C-acetyltransferase (EC 2.3.1.54) - cherichia coli   | 85      | 74     | 273  |
|        | 3111 | 1     | 595    | 299       | gi 633568        | limb deformity protein [Gallus gallus]  | 85      | 85     | 297  |
|        | 3778 | 1     | 630    | 316       | gi 3991840       | lbeta-subunit of HDT [Pseudomonas fragi]  | 85      | 67     | 315  |
|        | 3835 | 1     | 1      | 387       | gi 1204472       | type I restriction enzyme ECOR124/3 I M protein [Haemophilus influenzae]  | 85      | 56     | 387  |
|        | 4042 | 1     | 3      | 386       | gi 18178         | formate acetyltransferase [Chlamydomonas reinhardtii] ir S24997 S24997<br>  formate C-acetyltransferase (EC 2.3.1.54) - lamydomonas reinhardtii                                       | 85      | 70     | 384  |
|        | 4053 | 1     | 35     | 340       | gi 1204472       | type I restriction enzyme ECOR124/3 I M protein [Haemophilus influenzae]  | 85      | 56     | 306  |
|        | 4108 | 1     | 2      | 181       | gi 1072418       | lgcA gene product [Staphylococcus carnosus]   | 85      | 61     | 180  |
|        | 4300 | 1     | 575    | 330       | gi 151932        | fructose enzyme II [Rhodobacter capsulatus]   | 85      | 59     | 246  |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop   | match       | match gene name   | % sim  | % ident | length |
|--------|-----|--------|--------|-------------|---|--|---------|--------|
| ID     | ID  | (nt)   | (nt)   | accession   |   | (nt)   | (nt)    |        |
| 4392   | 1   | 1      | 627    | 355         | lgi 1022725   | unknown [Staphylococcus haemolyticus]  | 1       | 85     |
| 4408   | 1   | 1      | 2      | 235         | lgi 871784  | Clp-like ATP-dependent protease binding subunit [Bos taurus]   | 1       | 85     |
| 4430   | 1   | 1      | 578    | 291         | lgi 1009366   | Respiratory nitrate reductase [Bacillus subtilis]  | 1       | 85     |
| 4555   | 1   | 1      | 2      | 253         | lgi 450688  | hsdM gene of Ecoprr1 gene product [Escherichia coli] piri S38437 S38437 hsdM protein - Escherichia coli [SUB 40-520] | 1       | 85     |
| 4611   | 1   | 1      | 481    | 242         | lgi 1256635   | dihydroxy-acid dehydratase [Bacillus subtilis]   | 1       | 85     |
| 4      | 10  | 110061 | 110591 | lgi 46982   | fosB gene product [Staphylococcus epidermidis]                      | 1  | 84      | 65     |
| 13     | 2   | 1      | 1348   | 1172        | lgi 142450  | ahrC protein [Bacillus subtilis]   | 1       | 84     |
| 16     | 4   | 1      | 1803   | 4652        | lgi 1277198   | DNA repair protein [Deinococcus radiodurans]   | 1       | 84     |
| 22     | 3   | 1      | 1535   | 1128        | lgi 1511069   | UreF [Staphylococcus xylosus]  | 1       | 84     |
| 23     | 7   | 1      | 5055   | 5306        | lgi 603320  | Yer082p [Saccharomyces cerevisiae]   | 1       | 84     |
| 53     | 111 | 111597 | 11145  | lgi 1303948 | YqiW [Bacillus subtilis]  | 1  | 84      | 68     |
| 53     | 112 | 114059 | 112770 | lgi 142613  | branched chain alpha-keto acid dehydrogenase E2 [Bacillus subtilis] | 1  | 84      | 453    |
| 70     | 1   | 1      | 1332   | 982         | lgi 464647  | lgi 1303944 BfmBB [Bacillus subtilis]  | 1       | 84     |
| 73     | 4   | 1      | 2512   | 4311        | lgi 142993  | ORF (repE) [Staphylococcus aureus]   | 1       | 84     |
| 98     | 7   | 1      | 4324   | 6096        | lgi 467427  | glycerol-3-phosphate dehydrogenase (glpD) (EC 1.1.99.5) [Bacillus subtilis]  | 1       | 84     |
| 100    | 9   | 1      | 9501   | 8680        | lgi 1340128   | l-methionyl-tRNA synthetase [Bacillus subtilis]  | 1       | 84     |
| 117    | 3   | 1      | 1934   | 3208        | lgi 1237019   | ORF1 [Staphylococcus aureus]   | 1       | 84     |
| 148    | 6   | 1      | 4720   | 5670        | lgi 467462  | Srb [Bacillus subtilis]  | 1       | 84     |
| 152    | 4   | 1      | 2064   | 2456        | lgi 143377  | cysteine synthetase A [Bacillus subtilis]  | 1       | 84     |
| 169    | 7   | 1      | 3634   | 3861        | lgi 1001342   | pyruvate decarboxylase (E-1) alpha subunit [Bacillus subtilis] (EC 1.2.4.1) lpha chain - Bacillus subtilis           | 1       | 84     |
| 171    | 4   | 1      | 2992   | 2657        | lgi 517475  | hypothetical protein [Synechocystis sp.]   | 1       | 84     |
| 186    | 6   | 1      | 6941   | 6216        | lgi 467475  | D-amino acid transaminase [Staphylococcus haemolyticus]  | 1       | 84     |
| 205    | 9   | 1      | 6261   | 5692        | lgi 216340  | unknown [Bacillus subtilis]  | 1       | 84     |
| 224    | 2   | 1      | 915    | 1391        | lgi 288269  | ORF for adenylyl kinase [Bacillus subtilis]  | 1       | 84     |
|        |     |        |        |             |   | beta-fructofuranosidase [Staphylococcus xylosus]   | 1       | 84     |

| Contig | ORF | Start | Stop | match           | match gene name   | % sim   | % ident | length |     |
|--------|-----|-------|------|-----------------|---|---|---------|--------|-----|
| ID     | ID  | (nt)  | (nt) | accession       |   | (nt)  | (nt)    | (nt)   |     |
| 251    | 1   | 92    | 388  | gi 1303790      | YqeI [Bacillus subtilis]  | 84  | 65      | 297    |     |
| 282    | 3   | 1526  | 2836 | gi 143040       | glutamate-1-semialdehyde 2,1-aminotransferase [Bacillus subtilis]<br>pir D42728 D42728 glutamate-1-semialdehyde 2,1-aminotransferase (EC .4.3.8) -<br>Bacillus subtilis | 84  | 75      | 1311   |     |
| 307    | 5   | 3138  | 2959 | gi 1070014      | protein-dependent [Bacillus subtilis]   | 84  | 62      | 180    |     |
| 320    | 4   | 2343  | 4229 | gi 143390       | carbamyl phosphate synthetase [Bacillus subtilis]   | 84  | 70      | 1887   |     |
| 372    | 1   | 3     | 296  | gi 1022725      | unknown [Staphylococcus haemolyticus]   | 84  | 70      | 294    |     |
| 413    | 2   | 2201  | 1341 | gi 1256146      | YbbQ [Bacillus subtilis]  | 84  | 65      | 861    |     |
| 439    | 1   | 3     | 392  | gi 1046173      | osmotically inducible protein [Mycoplasma genitalium]   | 84  | 53      | 390    |     |
| 461    | 3   | 1362  | 2270 | gi 40211        | threonine synthase (thrc) (AA 1-352) [Bacillus subtilis] ir A25364 A25364<br>threonine synthase (EC 4.2.99.2) - Bacillus subtilis                                       | 84  | 69      | 909    |     |
| 487    | 1   | 1     | 3    | 299             | integrin-like protein alpha Int1p [Candida albicans]  | 84  | 46      | 297    |     |
| 491    | 2   | 624   | 905  | pir S08564 R3BS | ribosomal protein S9 - Bacillus stearothermophilus  | 84  | 69      | 282    |     |
| 491    | 3   | 1     | 836  | pir S08564 R3BS | ribosomal protein S9 - Bacillus stearothermophilus  | 84  | 77      | 198    |     |
| 548    | 1   | 1     | 3    | 341             | gi 431231   | uracil permease [Bacillus caldolyticus]                     | 84      | 74     | 339 |
| 728    | 2   | 2701  | 1748 | gi 912445       | 1DNA polymerase [Bacillus caldovenax]   | 84  | 68      | 954    |     |
| 769    | 1   | 1     | 3    | 257             | gi 1510953  | cobalamin biosynthesis protein N [Methanococcus jannaschii] | 84      | 38     | 255 |
| 954    | 1   | 308   | 156  | gi 1405454      | aconitase [Bacillus subtilis]   | 84  | 57      | 153    |     |
| 957    | 1   | 3     | 395  | gi 143402       | recombination protein (ttg start codon) [Bacillus subtilis] gi 1303923 RecN   | 84  | 68      | 393    |     |
| 1585   | 1   | 1     | 3    | 257             | gi 510140   | lipoendopeptidase F [Lactococcus lactis]                    | 84      | 70     | 450 |
| 2954   | 1   | 3     | 323  | gi 603769       | HutU protein, urocanase [Bacillus subtilis]   | 84  | 73      | 321    |     |
| 2996   | 1   | 650   | 348  | gi 18178        | formate acetyltransferase [Chlamydomonas reinhardtii] ir S24997 S21997<br>formate C-acetyltransferase (EC 2.3.1.54) - Chlamydomonas reinhardtii                         | 84  | 65      | 303    |     |
| 3766   | 1   | 737   | 375  | gi 517205       | 67 kDa Myosin-crossreactive streptococcal antigen [Streptococcus ssp. ssp.]   | 84  | 72      | 363    |     |
| 4022   | 1   | 2     | 169  | gi 1146206      | glutamate dehydrogenase [Bacillus subtilis]   | 84  | 54      | 168    |     |
| 4058   | 1   | 620   | 312  | gi 151932       | fructose enzyme II [Rhodobacter capsulatus]   | 84  | 71      | 309    |     |
| 4108   | 2   | 106   | 351  | gi 1072418      | glcA gene product [Staphylococcus carnosus]   | 84  | 77      | 246    |     |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop | match     | match gene name | % sim  | % ident  | length |      |      |
|--------|-----|--------|------|-----------|-----------------|--|--|--------|------|------|
| ID     | ID  | (nt)   | (nt) | accession |                 | (nt)   |  | (nt)   |      |      |
| 4183   | 1   | 1      | 3    | 308       | gi 603769       | HutU protein, urocanase [Bacillus subtilis]  | 84   | 72     | 306  |      |
| 4726   | 1   | 1      | 55   | 234       | gi 146208       | glutamate synthase large subunit (EC 2.6.1.53) [Escherichia coli]<br>pir A29617 A29617 glutamate synthase (NADPH) (EC 1.4.1.13) large chain - Escherichia coli | 84   | 73     | 180  |      |
| 22     | 4   | 2043   | 1    | 1576      | gi 393297       | lurease accessory protein [Bacillus sp.]   | 83   | 64     | 468  |      |
| 53     | 13  | 14722  | 1    | 13745     | gi 142612       | lbranched chain alpha-keto acid dehydrogenase E1-beta [Bacillus subtilis]  | 83   | 68     | 978  |      |
| 57     | 16  | 113357 | 1    | 12872     | gi 143132       | lactate dehydrogenase (AC 1.1.1.27) [Bacillus caldolyticus]<br>pir B29704 B29704 L-lactate dehydrogenase (EC 1.1.1.27) - Bacillus caldolyticus                 | 83   | 66     | 486  |      |
| 66     | 3   | 3119   | 1    | 2274      | gi 1303894      | lYqhM [Bacillus subtilis]  | 83   | 63     | 846  |      |
| 66     | 5   | 6118   | 1    | 4643      | gi 1212730      | lYqhK [Bacillus subtilis]  | 83   | 68     | 1476 |      |
| 70     | 3   | 1864   | 1    | 1523      | gi 44095        | replication initiator protein [Listeria monocytogenes]   | 83   | 73     | 342  |      |
| 90     | 1   | 377    | 1    | 1429      | gi 155571       | lalcohol dehydrogenase I (adhA) (EC 1.1.1.1) [Zymomonas mobilis]<br>pir A35260 A35260 alcohol dehydrogenase (EC 1.1.1.1) I - Zymomonas mobilis                 | 83   | 70     | 1053 |      |
| 95     | 2   | 708    | 1    | 2162      | gi 506381       | lphospho-beta-glucosidase [Bacillus subtilis]  | 83   | 70     | 1455 |      |
| 137    | 1   | 68     | 1    | 694       | gi 467391       | linitiation protein of replicaton [Bacillus subtilis]  | 83   | 77     | 627  |      |
| 140    | 4   | 13209  | 1    | 2742      | gi 634107       | lkdpB [Escherichia coli]   | 83   | 65     | 468  |      |
| 142    | 3   | 3468   | 1    | 2989      | gi 1212776      | lumazine synthase (b-subunit) [Bacillus amyloliquefaciens]   | 83   | 69     | 480  |      |
| 161    | 12  | 1      | 5749 | 1         | 6696            | gi 903307  | lORF75 [Bacillus subtilis]   | 83     | 64   | 948  |
| 164    | 9   | 1      | 9880 | 1         | 11070           | gi 49316   | lORF2 gene product [Bacillus subtilis]                                     | 83     | 66   | 1191 |
| 164    | 14  | 14148  | 1    | 14546     | gi 1580902      | lORF6 gene product [Bacillus subtilis]   | 83   | 60     | 399  |      |
| 170    | 2   | 1      | 3144 | 1         | 2467            | gi 520844  | lorf4 [Bacillus subtilis]  | 83     | 64   | 678  |
| 186    | 2   | 1      | 2029 | 1         | 1370            | gi 289284  | lcysteinyl-tRNA synthetase [Bacillus subtilis]                             | 83     | 72   | 660  |
| 205    | 14  | 1      | 7822 | 1         | 7607            | gi 216337  | lORF for L30 ribosomal protein [Bacillus subtilis]                         | 83     | 74   | 216  |
| 237    | 6   | 1      | 3683 | 1         | 4540            | gi 1510488   | limidazoleglycerol-phosphate synthase (cyclase) [Methanococcus jannaschii] | 83     | 60   | 858  |
| 301    | 1   | 1      | 985  | 1         | 638             | gi 467419  | lunknown [Bacillus subtilis]   | 83     | 65   | 348  |
| 302    | 4   | 1      | 1421 | 1         | 2743            | gi 508979  | lGTP-binding protein [Bacillus subtilis]                                   | 83     | 68   | 1323 |
| 321    | 4   | 1      | 3933 | 1         | 3571            | gi 39844   | lfumarase (citG) (aa 1-462) [Bacillus subtilis]                            | 83     | 68   | 363  |
| 367    | 1   | 1      | 2    | 1         | 352             | gi 1039479   | lOREU [Lactococcus lactis]   | 83     | 54   | 351  |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop  | match      | gene name   | % sim | % ident | length |
|--------|-----|--------|-------|------------|---|-------|---------|--------|
| ID     | ID  | (nt)   | (nt)  | accession  |   | (nt)  |         | (nt)   |
| 387    | 1   | 1      | 3     | 662        | gi 1806281  | 1     | 83      | 70     |
| 527    | 2   | 916    | 1566  | gi 396259  | DNA polymerase I [Bacillus stearothermophilus]<br> protease [Staphylococcus epidemidis]   | 1     | 83      | 67     |
| 533    | 1   | 355    | 179   | gi 142455  | alanine dehydrogenase (EC 1.4.1.1) [Bacillus stearothermophilus]<br> pir B34261 B34261 alanine dehydrogenase (EC 1.4.1.1) - Bacillus<br> stearothermophilus | 1     | 83      | 66     |
| 536    | 4   | 1617   | 1438  | gi 143366  | adenylosuccinate lyase (PUR-B) [Bacillus subtilis] pir C29326 WZBSDS  | 1     | 83      | 67     |
| 652    | 1   | 2      | 859   | gi 520753  | adenylosuccinate lyase (EC 4.3.2.2) - Bacillus subtilis   | 1     | 83      | 72     |
| 774    | 2   | 200    | 361   | gi 1522665 | DNA topoisomerase I [Bacillus subtilis]   | 1     | 83      | 58     |
| 897    | 1   | 120    | 296   | gi 1064807 | M. jannaschii predicted coding region MJECL28 [Methanococcus jannaschii]  | 1     | 83      | 162    |
| 1213   | 1   | 3      | 491   | gi 289288  | ORTHININE AMINOTRANSFERASE [Bacillus subtilis]<br> lexA [Bacillus subtilis]   | 1     | 83      | 76     |
| 2529   | 1   | 296    | 150   | gi 143786  | tryptophanyl-tRNA synthetase (EC 6.1.1.2) [Bacillus subtilis]<br> pir JT0481 YWB5 tryptophanyl-tRNA ligase (EC 6.1.1.2) - Bacillus subtilis                 | 1     | 83      | 177    |
| 2973   | 1   | 649    | 326   | gi 1109687 | ProZ [Bacillus subtilis]  | 1     | 83      | 67     |
| 3009   | 1   | 728    | 366   | gi 882532  | ORF_O294 [Escherichia coli]   | 1     | 83      | 489    |
| 3035   | 2   | 45     | 305   | gi 950062  | hypothesetical Yeast protein 1 [Mycoplasma capricolum] pir S48578 S48578<br> hypothetical protein - Mycoplasma capricolum SGC3) (fragment)                  | 1     | 83      | 324    |
| 3906   | 1   | 67     | 309   | gi 1353197 | thioredoxin reductase [Eubacterium acidaminophilum]   | 1     | 83      | 59     |
| 4458   | 1   | 540    | 271   | gi 397526  | clumping factor [Staphylococcus aureus]   | 1     | 83      | 261    |
| 4570   | 1   | 444    | 223   | gi 1022726 | unknown [Staphylococcus haemolyticus]   | 1     | 83      | 243    |
| 4654   | 1   | 97     | 261   | gi 1072419 | glcB gene product [Staphylococcus carnosus]   | 1     | 83      | 78     |
| 16     | 2   | 295    | 1191  | gi 153854  | lvs402 protein [Streptococcus pneumoniae]   | 1     | 82      | 222    |
| 16     | 3   | 1193   | 1798  | gi 153854  | lvs402 protein [Streptococcus pneumoniae]   | 1     | 82      | 165    |
| 38     | 12  | 9644   | 8724  | gi 1204400 | N-acetylneuraminate lyase [Haemophilus influenzae]  | 1     | 82      | 70     |
| 42     | 4   | 988    | 2019  | gi 841192  | catalase [Bacteroides fragilis]   | 1     | 82      | 921    |
| 51     | 6   | 2590   | 3489  | gi 143607  | sporulation protein [Bacillus subtilis]   | 1     | 82      | 1032   |
| 56     | 11  | 112270 | 13925 | gi 39431   | oligo-1,6-glucosidase [Bacillus cereus]   | 1     | 82      | 69     |
| 56     | 15  | 117673 | 18014 | gi 467410  | unknown [Bacillus subtilis]   | 1     | 82      | 342    |
| 61     | 2   | 881    | 3313  | gi 143148  | transfer RNA-Ile synthetase [Bacillus subtilis]   | 1     | 82      | 2433   |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop   | match           | match gene name   | % sim | % ident | length |
|--------|-----|-------|--------|-----------------|---|-------|---------|--------|
| ID     | ID  | (nt)  | (nt)   | accession       |   | (nt)  | (nt)    | (nt)   |
| 82     | 7   | 9162  | 11318  | gi 48240        | elongation factor G (AA 1-691) [Thermus aquaticus thermophilus]<br>  ir S15928 EFTWG translation elongation factor G - Thermus aquaticus<br>  p P13551 BFG_ THETH ELONGATION FACTOR G (EF-G).   | 82    | 64      | 2157   |
| 85     | 2   | 5470  | 3260   | gi 143369       | phosphoribosylformyl glycaminidine synthetase II (PUR-Q) [Bacillus subtilis]  | 82    | 66      | 2211   |
| 102    | 6   | 3662  | 5380   | gi 1256635      | dihydroxy-acid dehydratase [Bacillus subtilis]  | 82    | 65      | 1719   |
| 117    | 4   | 3242  | 3493   | pir A47154 A471 | orf1 5' of Ffh - Bacillus subtilis  | 82    | 53      | 252    |
| 128    | 6   | 4377  | 5933   | gi 460258       | phosphoglycerate mutase [Bacillus subtilis]   | 82    | 66      | 1557   |
| 129    | 2   | 1229  | 2182   | gi 403373       | glycerophosphoryl diester phosphodiesterase [Bacillus subtilis]<br>  pir S37251 S37251 glycerophosphoryl diester phosphodiesterase - acillus<br>  subtilis  | 82    | 62      | 954    |
| 170    | 1   | 2     | 1441   | gi 1377831      | unknown [Bacillus subtilis]   | 82    | 67      | 1440   |
| 177    | 1   | 3     | 1094   | gi 467386       | thiophen and furan oxidation [Bacillus subtilis]  | 82    | 65      | 1092   |
| 184    | 4   | 3572  | 4039   | gi 153566       | ORF (19K protein) [Enterococcus faecalis]   | 82    | 59      | 468    |
| 189    | 8   | 4455  | 4225   | gi 1001878      | ICSP1 protein [Listeria monocytogenes]  | 82    | 73      | 231    |
| 206    | 19  | 21366 | 120707 | gi 473916       | lipopeptide antibiotics iturin A [Bacillus subtilis] sp P39144 LIP14_BACSU<br>  LIPOPEPTIDE ANTIBIOTICS ITURIN A AND SURFACTIN IOSYNTHESIS PROTEIN.   | 82    | 50      | 660    |
| 221    | 2   | 805   | 1722   | gi 517205       | 167 kDa Myosin-crossreactive streptococcal antigen [Streptococcus yogenes]  | 82    | 63      | 918    |
| 223    | 4   | 3866  | 3651   | gi 439619       | [Salmonella typhimurium IS200 insertion sequence from SARA17, artial.],<br>  gene product [Salmonella typhimurium]  | 82    | 69      | 216    |
| 260    | 3   | 5207  | 4296   | gi 1161381      | IcaB [Staphylococcus epidermidis]   | 82    | 61      | 912    |
| 315    | 3   | 4864  | 2855   | gi 143397       | lquinol oxidase [Bacillus subtilis]   | 82    | 67      | 2010   |
| 321    | 10  | 8520  | 7945   | gi 142981       | ORF5; This ORF includes a region (aa23-103) containing a potential ron-<br>  sulphur centre homologous to a region of Rhodospirillum rubrum rd<br>  Chromatium vinosum; putative [Bacillus stearothermophilus]<br>  pir PQ0299 PQ0299 hypothetical protein 5 (gldA 3' region) - | 82    | 62      | 576    |
| 331    | 3   | 1055  | 1342   | gi 436574       | ribosomal protein L1 [Bacillus subtilis]  | 82    | 71      | 288    |
| 370    | 2   | 262   | 618    | gi 1303793      | YqEL [Bacillus subtilis]  | 82    | 59      | 357    |
| 404    | 4   | 3053  | 4024   | gi 1303821      | YqfE [Bacillus subtilis]  | 82    | 68      | 972    |
| 405    | 4   | 4440  | 3073   | gi 1303913      | YqfX [Bacillus subtilis]  | 82    | 67      | 1368   |
| 436    | 3   | 4096  | 2864   | gi 149521       | tryptophan synthase beta subunit [Lactococcus lactis] pir S35129 S35129<br>  tryptophan synthase (EC 4.2.1.20) beta chain - actococcus lactis subsp.<br>  lactis  | 82    | 67      | 1233   |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop  | match      | gene name  | % sim | % ident | length |
|--------|-----|-------|-------|------------|--|-------|---------|--------|
| ID     | ID  | (nt)  | (nt)  | accession  |  | (nt)  | (nt)    |        |
| 441    | 4   | 3394  | 2573  | gi 142952  | glyceraldehyde-3-phosphate dehydrogenase [Bacillus stearothermophilus]   | 82    | 67      | 822    |
| 444    | 12  | 10415 | 11227 | gi 1204354 | lspore germination and vegetative growth protein [Haemophilus influenzae]  | 82    | 67      | 813    |
| 446    | 1   | 3     | 191   | gi 143387  | aspartate transcarbamylase [Bacillus subtilis]   | 82    | 66      | 189    |
| 462    | 3   | 1007  | 1210  | gi 142521  | deoxyribodipyrimidine photolyase [Bacillus subtilis] pir A37192 B37192 uvrB protein - Bacillus subtilis sp P14951 UVRC_BACSU EXCINUCLEASE ABC SUBUNIT C. | 82    | 64      | 204    |
| 537    | 1   | 1560  | 784   | gi 853767  | [UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus subtilis]   | 82    | 61      | 777    |
| 680    | 2   | 407   | 700   | gi 426472  | lsecE gene product [Staphylococcus carnosus]   | 82    | 69      | 294    |
| 724    | 2   | 565   | 386   | gi 143373  | phosphoribosyl aminoimidazole carboxy formyl ormyltransferase/inosine monophosphate cyclohydrolase (PUR-H(J)) Bacillus subtilis                          | 82    | 68      | 180    |
| 763    | 1   | 422   | 213   | gi 467458  | cell division protein [Bacillus subtilis]  | 82    | 35      | 210    |
| 818    | 1   | 564   | 283   | gi 1064787 | function unknown [Bacillus subtilis]   | 82    | 69      | 282    |
| 858    | 1   | 175   | 1176  | gi 143043  | luroporphyrinogen decarboxylase [Bacillus subtilis] pir B47045 B47045  | 82    | 71      | 1002   |
| 895    | 1   | 3     | 599   | gi 1027507 | luroporphyrinogen decarboxylase (EC 4.1.1.37) - acillus subtilis   | 82    | 72      | 597    |
| 939    | 1   | 10    | 399   | gi 143795  | ATP binding protein [Borrelia burgdorferi]   | 82    | 60      | 390    |
| 961    | 1   | 1     | 306   | gi 577647  | transfer RNA-Tyr synthetase [Bacillus subtilis]  | 82    | 69      | 306    |
| 1192   | 1   | 307   | 155   | gi 146974  | gamma-hemolysin [Staphylococcus aureus]  | 82    | 71      | 153    |
| 1317   | 1   | 49    | 375   | gi 407908  | NH3-dependent NAD synthetase [Escherichia coli]  | 82    | 72      | 327    |
| 1341   | 1   | 1     | 150   | gi 39962   | lEIiscr [Staphylococcus xylosus]   | 82    | 68      | 150    |
| 2990   | 2   | 567   | 349   | gi 534855  | lATPase subunit epsilon [Bacillus stearothermophilus] sp P42009 ATPE_BACST   | 82    | 47      | 219    |
| 3024   | 1   | 45    | 224   | gi 467402  | lunkown [Bacillus subtilis]  | 82    | 64      | 180    |
| 3045   | 1   | 1     | 276   | gi 467335  | ribosomal protein L9 [Bacillus subtilis]   | 82    | 60      | 138    |
| 3045   | 2   | 558   | 400   | gi 467335  | ribosomal protein L9 [Bacillus subtilis]   | 82    | 82      | 159    |
| 3091   | 1   | 474   | 238   | gi 499335  | lsecA protein [Staphylococcus carnosus]  | 82    | 78      | 237    |
| 3107   | 1   | 416   | 210   | gi 546918  | lorfY 3' of comK [Bacillus subtilis, E26, Peptide Partial, 140 aa]   | 82    | 64      | 207    |
|        |     |       |       |            | pir S43612 S43612 hypothetical protein Y - Bacillus subtilis   |       |         |        |
|        |     |       |       |            | sp P40398 YHxD_BACSU HYPOTHETICAL PROTEIN IN COMK 3' REGION (ORFY FRAGMENT)  |       |         |        |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop  | match<br>accession | match<br>gene name | % sim  | % ident | length<br>(nt) |      |
|--------|-----|-------|-------|--------------------|--------------------|--|---------|----------------|------|
| ID     | ID  | (nt)  | (nt)  |                    |                    |  |         |                |      |
| 4332   | 1   | 1     | 2     | 319                | gi 42086           | nitrate reductase alpha subunit [Escherichia coli] pIP09152 NARG_ECOLI   | 82      | 75             | 318  |
|        |     |       |       |                    |                    | RESPIRATORY NITRATE REDUCTASE 1 ALPHA CHAIN (EC 7.99.4). (SUB 2-1247)  |         |                |      |
| 23     | 3   | 1     | 3275  | 2574               | gi 1199573         | lspB [Sphingomonas sp.]  | 81      | 64             | 702  |
|        |     |       |       |                    |                    | lysine specific permease [Escherichia coli]  | 81      | 59             | 318  |
| 42     | 1   | 1     | 638   | 321                | gi 466778          | IM. genitalium predicted coding region MG246 [Mycoplasma genitalium]   | 81      | 62             | 300  |
|        |     |       |       |                    |                    |  | 81      | 55             | 1002 |
| 48     | 5   | 1     | 4051  | 4350               | gi 1045937         | laciAC protein - Bacillus subtilis   | 81      | 67             | 1131 |
|        |     |       |       |                    |                    |  | 81      | 66             | 1449 |
| 51     | 4   | 1     | 1578  | 2579               | pir S16649 S166    | laciAC protein - Bacillus subtilis   | 81      | 65             | 1002 |
|        |     |       |       |                    |                    |  | 81      | 64             | 1575 |
| 53     | 2   | 1     | 364   | 1494               | gi 1303961         | lYqjJ [Bacillus subtilis]  | 81      | 74             | 618  |
|        |     |       |       |                    |                    | 6-phosphogluconate dehydrogenase [Escherichia coli]  | 81      | 70             | 372  |
| 53     | 8   | 1     | 9419  | 7971               | gi 146930          | lpermease [Bacillus subtilis]  | 81      | 65             | 639  |
|        |     |       |       |                    |                    |  | 81      | 64             | 1578 |
| 54     | 9   | 1     | 10757 | 10119              | gi 143016          | lgluconate kinase [Bacillus subtilis]  | 81      | 64             | 1062 |
|        |     |       |       |                    |                    |  | 81      | 63             | 1062 |
| 54     | 10  | 1     | 13360 | 11786              | gi 143015          | lNifU-related protein [Haemophilus influenzae]   | 81      | 54             | 492  |
|        |     |       |       |                    |                    |  | 81      | 53             | 492  |
| 57     | 117 | 1     | 13983 | 113366             | pir A25805 A258    | lL-lactate dehydrogenase (EC 1.1.1.27) - Bacillus subtilis   | 81      | 74             | 618  |
|        |     |       |       |                    |                    |  | 81      | 70             | 372  |
| 81     | 2   | 1     | 2708  | 2217               | gi 1222302         | lipa-93d gene product [Bacillus subtilis]  | 81      | 64             | 1578 |
|        |     |       |       |                    |                    |  | 81      | 63             | 1578 |
| 86     | 1   | 1     | 745   | 374                | gi 414017          | lipa-93d gene product [Bacillus subtilis]  | 81      | 64             | 1578 |
|        |     |       |       |                    |                    |  | 81      | 63             | 1578 |
| 103    | 6   | 1     | 6438  | 4861               | gi 971342          | lnitrate reductase beta subunit [Bacillus subtilis] sp P42176 NARH_BACSU                                       | 81      | 64             | 1578 |
|        |     |       |       |                    |                    |  | 81      | 63             | 1578 |
| 120    | 115 | 1     | 10845 | 112338             | gi 1524392         | lgbsA [Bacillus subtilis]  | 81      | 67             | 1494 |
|        |     |       |       |                    |                    |  | 81      | 66             | 1494 |
| 128    | 5   | 1     | 3676  | 4413               | gi 143319          | lriose phosphate isomerase [Bacillus megaterium]   | 81      | 64             | 738  |
|        |     |       |       |                    |                    |  | 81      | 63             | 738  |
| 131    | 9   | 1     | 10308 | 9280               | gi 299163          | lalanine dehydrogenase [Bacillus subtilis]   | 81      | 68             | 1029 |
|        |     |       |       |                    |                    |  | 81      | 67             | 1029 |
| 143    | 6   | 1     | 6088  | 5471               | gi 439619          | l[Salmonella typhimurium IS200 insertion sequence from SARA17, artial.], gene product [Salmonella typhimurium] | 81      | 61             | 618  |
|        |     |       |       |                    |                    |  | 81      | 60             | 618  |
| 169    | 1   | 1     | 43    | 825                | gi 897795          | l30S ribosomal protein [Pediococcus acidilactici] sp P49668 RS2_PEDAC_30S                                      | 81      | 65             | 783  |
|        |     |       |       |                    |                    |  | 81      | 64             | 783  |
| 230    | 1   | 1     | 450   | 226                | gi 1125826         | lshort region of weak similarity to tyrosine-protein kinase receptors in a                                     | 81      | 54             | 225  |
|        |     |       |       |                    |                    |  | 81      | 53             | 225  |
| 233    | 5   | 1     | 2000  | 2677               | gi 467404          | lunknown [Bacillus subtilis]   | 81      | 63             | 678  |
|        |     |       |       |                    |                    |  | 81      | 62             | 678  |
| 241    | 2   | 1     | 3081  | 2149               | gi 16510           | lsuccinate--CoA ligase (GDP-forming) [Arabidopsis thaliana] ir S30579 S30579                                   | 81      | 69             | 933  |
|        |     |       |       |                    |                    |  | 81      | 68             | 933  |
|        |     |       |       |                    |                    |  | 81      | 67             | 933  |
| 256    | 1   | 1     | 1     | 981                | pir S09411 S094    | lspoIIIE protein - Bacillus subtilis   | 81      | 65             | 981  |
|        |     |       |       |                    |                    |  | 81      | 64             | 981  |
| 259    | 3   | 1     | 3752  | 2691               | sp P28367 RF2_B    | lPROBABLE PEPTIDE CHAIN RELEASE FACTOR 2 (RF-2) (FRAGMENT).  | 81      | 65             | 1062 |
|        |     |       |       |                    |                    |  | 81      | 64             | 1062 |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop | match           | match gene name  | % sim | % ident | length |
|--------|-----|-------|------|-----------------|--|-------|---------|--------|
| ID     | ID  | (nt)  | (nt) | accession       |  |       |         | (nt)   |
| 275    | 2   | 1728  | 3581 | gi 726480       | L-glutamine-D-fructose-6-phosphate amidotransferase [Bacillus subtilis]      | 81    | 68      | 1854   |
| 285    | 1   | 1466  | 1735 | gi 1204844      | H. influenzae predicted coding region H10594 [Haemophilus influenzae]        | 81    | 63      | 732    |
| 296    | 1   | 99    | 1406 | gi 467328       | adenylosuccinate synthetase [Bacillus subtilis]                              | 81    | 67      | 1308   |
| 302    | 9   | 5590  | 5889 | gi 147485       | lqueA [Escherichia coli]   | 81    | 64      | 300    |
| 317    | 2   | 1137  | 1376 | gi 154961       | lresolvase [Transposon Tn917]  | 81    | 51      | 240    |
| 343    | 2   | 1034  | 1342 | gi 405955       | lyeed [Escherichia coli]   | 81    | 60      | 309    |
| 360    | 2   | 1404  | 2471 | gi 1204570      | lasparyl-tRNA synthetase [Haemophilus influenzae]                            | 81    | 67      | 1068   |
| 364    | 5   | 6251  | 5706 | gi 1204652      | lmethylated-DNA--protein-cysteine methyltransferase [Haemophilus influenzae] | 81    | 63      | 546    |
| 372    | 2   | 1707  | 1135 | gi 467416       | lunkown [Bacillus subtilis]  | 81    | 65      | 573    |
| 392    | 1   | 43    | 603  | pir S09411 S094 | lspolIE protein - Bacillus subtilis  | 81    | 65      | 561    |
| 404    | 9   | 5252  | 6154 | gi 606745       | lBex [Bacillus subtilis]   | 81    | 65      | 903    |
| 426    | 2   | 1727  | 1119 | gi 39453        | lManganese superoxide dismutase [Bacillus caldotenax] ir S222053 S22053      | 81    | 66      | 609    |
| 480    | 7   | 5653  | 5889 | pir C37083 C370 | lhypothetical protein II (ompH 3' region) - Salmonella typhimurium           | 81    | 57      | 237    |
|        |     |       |      | l (fragment)    |  |       |         |        |
| 625    | 3   | 1105  | 2070 | gi 1262360      | lprotein kinase PknB [Mycobacterium leprae]                                  | 81    | 56      | 966    |
| 754    | 2   | 504   | 1064 | gi 1303902      | lyqHU [Bacillus subtilis]  | 81    | 71      | 561    |
| 842    | 1   | 86    | 430  | gi 1405446      | ltransketolase [Bacillus subtilis]   | 81    | 68      | 345    |
| 953    | 1   | 798   | 400  | gi 1205429      | ldipeptide transport ATP-binding protein [Haemophilus influenzae]            | 81    | 57      | 399    |
| 961    | 2   | 252   | 401  | gi 487686       | lsynergohymenotropic toxin [Staphylococcus intermedius] pir S44944 S44944    | 81    | 72      | 150    |
|        | 1   | 1     | 1    | 1               | lsynergohymenotropic toxin - Staphylococcus nternedius                       | 1     | 1       | 1      |
| 1035   | 1   | 1     | 189  | gi 1046138      | lM. genitalium predicted coding region MG423 [Mycoplasma genitalium]         | 81    | 43      | 189    |
| 1280   | 1   | 670   | 449  | gi 559164       | lhelicase [Autographa californica nuclear polyhedrosis virus]                | 81    | 43      | 222    |
|        | 1   | 1     | 1    | 1               | lsp P24307 V143_NPVAC HELICASE.  | 1     | 1       | 1      |
| 3371   | 1   | 68    | 241  | gi 1322245      | lmevalonate pyrophosphate decarboxylase [Rattus norvegicus]                  | 81    | 62      | 174    |
| 3715   | 1   | 475   | 239  | gi 537137       | lORF_f388 [Escherichia coli]   | 81    | 58      | 237    |
| 3908   | 1   | 2     | 325  | gi 439619       | l(Salmonella typhimurium IS200 insertion sequence from SARA17, artial.],     | 81    | 68      | 324    |
|        | 1   | 1     | 1    | 1               | l gene product [Salmonella typhimurium]                                      | 1     | 1       | 1      |
| 3940   | 1   | 3     | 401  | gi 296464       | lATPase (Lactococcus lactis)   | 81    | 69      | 399    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop   | match       | gene name   |  |
|--------|-----|--------|--------|-------------|---|--|
| ID     | ID  | (nt)   | (nt)   | accession   |   |  |
| 3954   | 1   | 1      | 318    | lgi 1224069 | lamiidase [Moraxella catarrhalis]   |  |
| 4049   | 1   | 337    | 170    | lgi 603768  | HutI protein, imidazolone-5-propionate hydrolase [Bacillus subtilis]<br>gi 603768 HutI protein, imidazolone-5-propionate hydrolase Bacillus subtilis] |  |
| 4209   | 1   | 1      | 324    | lgi 403373  | glycerophosphoryl diester phosphodiesterase [Bacillus subtilis]<br>pir S37231 S37251 glycerophosphoryl diester phosphodiesterase - acillus subtilis   |  |
| 4371   | 1   | 627    | 322    | lgi 2116677 | indolepyruvate decarboxylase [Enterobacter cloacae] pir S16013 S16013<br>indolepyruvate decarboxylase (EC 4.1.1.-) - nterobacter cloacae              |  |
| 4387   | 1   | 19     | 228    | lgi 460689  | lTVG [Thermoactinomyces vulgaris]   |  |
| 4391   | 1   | 581    | 306    | lgi 1524193 | lunkown [Mycobacterium tuberculosis]  |  |
| 4425   | 1   | 1      | 3      | lgi 143015  | lgluconate kinase [Bacillus subtilis]   |  |
| 9      | 1   | 1593   | 847    | lgi 1064786 | lfunction unknown [Bacillus subtilis]   |  |
| 17     | 1   | 544    | 311    | lgi 559164  | lhelicase [Autographa californica nuclear polyhedrosis virus]<br>sp P24307 V143_NPVAC HELICASE.   |  |
| 45     | 2   | 1159   | 2448   | lgi 1109684 | lProv [Bacillus subtilis]   |  |
| 45     | 5   | 4032   | 4733   | lgi 1109687 | lProZ [Bacillus subtilis]   |  |
| 54     | 8   | 110266 | 9502   | lgi 563952  | lgluconate permease [Bacillus licheniformis]  |  |
| 62     | 112 | 1      | 8852   | lgi 854655  | lNa/H antiporter system [Bacillus alcalophilus]   |  |
| 62     | 14  | 1      | 8087   | lgi 8683    | lORF [Homo sapiens]   |  |
| 67     | 116 | 113781 | 114122 | lgi 305002  | lORF f356 [Escherichia coli]  |  |
| 70     | 113 | 111495 | 110296 | lgi 1303995 | lYqkN [Bacillus subtilis]   |  |
| 98     | 1   | 9      | 63336  | lgi 467428  | lunkown [Bacillus subtilis]   |  |
| 98     | 110 | 1      | 7294   | lgi 7833    | lgi 467430  | lunkown [Bacillus subtilis]                            |
| 98     | 111 | 1      | 7820   | lgi 8737    | lgi 467431  | lhigh level kasugamycin resistance [Bacillus subtilis] |
| 109    | 116 | 14154  | 14813  | lgi 580875  | lipa-57d gene product [Bacillus subtilis]   |  |
| 112    | 115 | 14294  | 16636  | lgi 1072361 | lpyruvate-formate-lyase [Clostridium pasteurianum]  |  |
| 139    | 1   | 1      | 1448   | lgi 726     | lgi 506699  | lCapC [Staphylococcus aureus]                          |
| 139    | 2   | 2      | 2179   | lgi 1448    | lgi 506698  | lCapB [Staphylococcus aureus]                          |
| 174    | 4   | 3271   | 2870   | lgi 1146242 | laspارتate 1-decarboxylase [Bacillus subtilis]  |  |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop  | match       | match gene name   | % sim | % ident | length |
|--------|-----|--------|-------|-------------|---|-------|---------|--------|
| ID     | ID  | (nt)   | (nt)  | accession   |   | (nt)  | (nt)    |        |
| 177    | 3   | 2102   | 2842  | lgi 467385  | lunkown [Bacillus subtilis]   | 80    | 70      | 741    |
| 184    | 6   | 6124   | 5912  | lgi 161953  | 185-kDa surface antigen [Trypanosoma cruzi]                                 | 80    | 46      | 213    |
| 186    | 4   | 5368   | 3875  | lgi 289282  | l glutamyl-tRNA synthetase [Bacillus subtilis]                              | 80    | 65      | 1494   |
| 205    | 130 | 115796 | 15140 | lgi 40103   | ribosomal protein L4 [Bacillus stearothermophilus]                          | 80    | 66      | 657    |
| 207    | 1   | 140    | 1315  | lgi 460259  | lenolase [Bacillus subtilis]  | 80    | 67      | 1176   |
| 211    | 3   | 1078   | 1590  | lgi 410131  | ORFX7 [Bacillus subtilis]   | 80    | 61      | 513    |
| 235    | 2   | 1962   | 2255  | lgi 143797  | l valyl-tRNA synthetase [Bacillus stearothermophilus] sp P11931 SYV_BACST   | 80    | 55      | 294    |
| 239    | 1   | 1      | 1263  | lgi 143000  | \VALYL-TRNA SYNTHETASE (EC 6.1.1.9) VALINE--tRNA LIGASE) (VALRS).           |       |         |        |
| 301    | 3   | 1446   | 1111  | lgi 467418  | l proton glutamate symport protein [Bacillus stearothermophilus]            | 80    | 59      | 1263   |
| 301    | 5   | 2724   | 2461  | lgi 709993  | \pir S26247 S26247 glutamate/aspartate transport protein - Bacillus         |       |         |        |
| 301    | 4   | 5697   | 4501  | lgi 1177686 | hypothetical protein [Bacillus subtilis]                                    | 80    | 54      | 264    |
| 310    | 6   | 5258   | 7006  | lgi 348053  | l acuC gene product [Staphylococcus xylosus]                                | 80    | 58      | 336    |
| 310    | 7   | 7410   | 9113  | lgi 1103865 | \l acetyl-CoA synthetase [Bacillus subtilis]                                | 80    | 67      | 1197   |
| 325    | 3   | 1114   | 1389  | lgi 310325  | l formyl-tetrahydrofolate synthetase [Streptococcus mutans]                 | 80    | 40      | 1704   |
| 337    | 1   | 1268   | 636   | lgi 537049  | \ORF_0470 [Escherichia coli]  | 80    | 55      | 633    |
| 374    | 2   | 929    | 1228  | lgi 1405448 | l outer capsid protein [Rotavirus sp.]                                      | 80    | 70      | 300    |
| 375    | 5   | 3062   | 3331  | lgi 467448  | l unknown [Bacillus subtilis]   | 80    | 68      | 270    |
| 388    | 1   | 267    | 587   | lgi 1064791 | l function unknown [Bacillus subtilis]                                      | 80    | 65      | 321    |
| 394    | 1   | 9      | 659   | lgi 304976  | l matches PS00017: ATP_GTP_A and PS00301: EFACTOR_GTP; similar to longation | 80    | 65      | 651    |
| 456    | 1   | 625    | 1263  | lgi 1146183 | \factor G, Tet/M/TetO_tetracycline-resistance proteins Escherichia coli]    |       |         |        |
| 475    | 1   | 1      | 1     | lgi 1483545 | l putative [Bacillus subtilis]  | 80    | 65      | 639    |
| 544    | 2   | 1449   | 2240  | lgi 529754  | l beta-fructofuranosidase [Staphylococcus xylosus]                          | 80    | 66      | 654    |
| 622    | 4   | 1623   | 1871  | lgi 1483545 | l unknown [Mycobacterium tuberculosis]                                      | 80    | 65      | 249    |
| 719    | 1   | 1      | 1257  | lgi 1064791 | l function unknown [Bacillus subtilis]                                      | 80    | 68      | 1257   |
| 739    | 1   | 107    | 838   | lgi 666983  | l putative ATP binding subunit [Bacillus subtilis]                          | 80    | 61      | 732    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop | match           | match gene name   | % sim | % ident | length |
|--------|-----|-------|------|-----------------|---|-------|---------|--------|
| ID     | ID  | (nt)  | (nt) | accession       |   | (nt)  | (nt)    | (nt)   |
| 745    | 2   | 581   | 414  | gi 1511600      | coenzyme PQQ synthesis protein III [Methanococcus jannaschii]                 | 1     | 80      | 61     |
| 822    | 1   | 17    | 679  | gi 410141       | ORFX17 [Bacillus subtilis]  | 1     | 80      | 68     |
| 827    | 2   | 991   | 836  | gi 1205301      | leukotoxin secretion ATP-binding protein [Haemophilus influenzae]             | 1     | 80      | 54     |
| 1044   | 1   | 3     | 149  | gi 60632        | vp2 [Marburg virus]   | 1     | 80      | 55     |
| 1220   | 2   | 571   | 413  | pir A61072 EPSG | galliderm precursor - Staphylococcus gallinarum                               | 1     | 80      | 74     |
| 2519   | 1   | 75    | 275  | gi 147556       | dpj [Escherichia coli]  | 1     | 80      | 45     |
| 2947   | 1   | 503   | 279  | gi 1184680      | polynucleotide phosphorylase [Bacillus subtilis]                              | 1     | 80      | 62     |
| 3120   | 1   | 2     | 226  | gi 517205       | 167 kDa Myosin-crossreactive streptococcal antigen [Streptococcus yogenes]    | 1     | 80      | 65     |
| 3191   | 1   | 294   | 148  | gi 151259       | HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii] pir A44736 A44756     | 1     | 80      | 59     |
|        |     |       |      |                 | hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) Pseudomonas sp.             | 1     | 1       | 147    |
| 3560   | 2   | 285   | 434  | gi 1217130      | photosystem I core protein B [Synechococcus vulgaris]                         | 1     | 80      | 70     |
| 3655   | 1   | 47    | 346  | gi 415855       | ldeoxyribose aldolase [Mycoplasma hominis]                                    | 1     | 80      | 56     |
| 3658   | 2   | 324   | 584  | gi 551531       | 12-nitropropane dioxygenase [Williopsis saturnus]                             | 1     | 80      | 54     |
| 3769   | 1   | 798   | 400  | gi 1339950      | large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]      | 1     | 80      | 68     |
| 3781   | 1   | 692   | 348  | gi 166412       | NADH-glutamate synthase [Medicago sativa]                                     | 1     | 80      | 62     |
| 3988   | 1   | 48    | 287  | gi 1204696      | fructose-permease IIBC component [Haemophilus influenzae]                     | 1     | 80      | 69     |
| 4030   | 1   | 571   | 287  | gi 1009366      | Respiratory nitrate reductase [Bacillus subtilis]                             | 1     | 80      | 60     |
| 4092   | 1   | 547   | 275  | gi 1370207      | orf6 [Lactobacillus sake]   | 1     | 80      | 69     |
| 4103   | 1   | 680   | 342  | gi 39956        | lIGIC [Bacillus subtilis]   | 1     | 80      | 65     |
| 4231   | 1   | 692   | 348  | gi 289287       | UDP-glucose pyrophosphorylase [Bacillus subtilis]                             | 1     | 80      | 65     |
| 4265   | 1   | 595   | 299  | gi 603768       | HutI protein, imidazolone-5-propionate hydrolase [Bacillus subtilis]          | 1     | 80      | 63     |
|        |     |       |      |                 | gi 603768 HutI protein, imidazolone-5-propionate hydrolase Bacillus subtilis] | 1     | 1       | 345    |
| 4504   | 1   | 498   | 250  | gi 1339950      | large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]      | 1     | 80      | 68     |
| 2      | 6   | 5998  | 6798 | gi 535351       | Cody [Bacillus subtilis]  | 1     | 79      | 63     |
| 4      | 7   | 8295  | 7051 | gi 603768       | HutI protein, imidazolone-5-propionate hydrolase [Bacillus subtilis]          | 1     | 79      | 64     |
|        |     |       |      |                 | gi 603768 HutI protein, imidazolone-5-propionate hydrolase Bacillus subtilis] | 1     | 1       | 1245   |
| 25     | 6   | 5273  | 5515 | pir A36728 A367 | acyl carrier protein - Rhizobium meliloti                                     | 1     | 79      | 65     |
|        |     |       |      |                 |   | 1     | 243     |        |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop   | match      | gene name  | % sim | % ident | length |
|--------|-----|--------|--------|------------|--|-------|---------|--------|
| ID     | ID  | (nt)   | (nt)   | accession  |  | (nt)  |         | (nt)   |
| 59     | 2   | 1173   | 1424   | gi 147923  | lthreonine dehydratase 2 (EC 4.2.1.16) [Escherichia coli]  | 1     | 79      | 75     |
| 60     | 1   | 1      | 204    | gi 666115  | lorf1 upstream of glucose kinase [Staphylococcus xylosus] pir S52351 S52351  | 1     | 79      | 60     |
|        |     |        |        |            | hypothetical protein 1 - Staphylococcus xylosus  |       |         | 204    |
| 81     | 1   | 3002   | 1590   | gi 466882  | ppsl; B1496_C2_189 [Mycobacterium leprae]  | 1     | 79      | 64     |
| 85     | 7   | 7023   | 6505   | gi 143364  | lphosphoribosyl aminimidazole carboxylase I (PUR-E) [Bacillus subtilis]  | 1     | 79      | 60     |
| 89     | 6   | 5660   | 4554   | gi 144906  | lproduct homologous to E.coli thioredoxin reductase: J.Biol.Chem. 1988)  | 1     | 79      | 35     |
|        |     |        |        |            | 263:9015-9019, and to F52a protein of alkyl hydroperoxide reductase from S.typhimurium: J.Biol.Chem. (1990) 265:10535-10540; pen reading frame A [Clostridium pasteurianum]                        |       | 1107    |        |
| 102    | 11  | 7489   | 8571   | gi 143093  | lketol-acid reductoisomerase [Bacillus subtilis] sp P37253 ILVC_BACSU_KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86) ACETOHYDROXY-ACID ISOMEROREDUCTASE (ALPHA-KETO-BETA-HYDROXYLACIL EDUCTOISOMERASE). | 1     | 79      | 64     |
|        |     |        |        |            |  |       |         | 1083   |
| 102    | 14  | 111190 | 112563 | gi 149428  | lputative [Lactococcus lactis]   | 1     | 79      | 65     |
| 127    | 9   | 7792   | 9372   | gi 458688  | lPrfC/RF3 [Dichelobacter nodosus]  | 1     | 79      | 68     |
| 139    | 3   | 2540   | 1983   | gi 506697  | lCapA [Staphylococcus aureus]  | 1     | 79      | 55     |
| 144    | 2   | 1644   | 1156   | gi 1498296 | lpeptide methionine sulfoxide reductase [Streptococcus pneumoniae]   | 1     | 79      | 47     |
| 148    | 2   | 529    | 1098   | gi 467457  | lhypoxanthine-guanine phosphoribosyltransferase [Bacillus subtilis]  | 1     | 79      | 59     |
|        |     |        |        |            | gi 467457 hypoxanthine-guanine phosphoribosyltransferase [Bacillus subtilis]   |       |         | 570    |
| 150    | 1   | 965    | 1591   | gi 755602  | lunknown [Bacillus subtilis]   | 1     | 79      | 61     |
| 176    | 1   | 1039   | 587    | gi 297874  | lfructose-bisphosphate aldolase [Staphylococcus carnosus] pir A49913 A49943  | 1     | 79      | 65     |
|        |     |        |        |            | fructose-bisphosphate aldolase (EC 4.1.2.13) - taphylococcus carnosus (strain TM300)   |       |         | 453    |
| 186    | 7   | 7584   | 6874   | gi 1314298 | lORF5; putative Sms protein; similar to Sms proteins from Haemophilus influenzae and Escherichia coli [Listeria monocytogenes]   | 1     | 79      | 64     |
|        |     |        |        |            |  |       |         | 711    |
| 205    | 116 | 8887   | 8498   | gi 1044980 | lribosomal protein L18 [Bacillus subtilis]   | 1     | 79      | 70     |
|        |     |        |        |            |  |       |         | 390    |
| 211    | 1   | 1      | 519    | gi 1303994 | lYqkM [Bacillus subtilis]  | 1     | 79      | 62     |
| 223    | 2   | 4183   | 2801   | gi 488430  | lalcohol dehydrogenase 2 [Entamoeba histolytica]   | 1     | 79      | 60     |
| 243    | 8   | 8915   | 7896   | gi 580883  | lipa-88d gene product [Bacillus subtilis]  | 1     | 79      | 60     |
|        |     |        |        |            |  |       |         | 1020   |
| 279    | 4   | 3721   | 4329   | gi 413930  | lipa-6d gene product [Bacillus subtilis]   | 1     | 79      | 59     |
| 300    | 1   | 11     | 1393   | gi 403372  | lglycerol 3-phosphate permease [Bacillus subtilis]   | 1     | 79      | 62     |
|        |     |        |        |            |  |       |         | 1383   |
| 307    | 3   | 2930   | 1935   | gi 950062  | lhypothetical yeast protein 1 [Mycoplasma capricolum] pir S48578 S48578  | 1     | 79      | 60     |
|        |     |        |        |            | hypothetical protein - Mycoplasma capricolum SGC3) (fragment)  |       |         | 996    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop | match           | match gene name   | % sim | % ident | length |
|--------|-----|--------|------|-----------------|---|-------|---------|--------|
| ID     | ID  | (nt)   | (nt) | accession       |   | (nt)  | (nt)    |        |
| 352    | 6   | 110106 | 1886 | gi 216854       | P47K [Pseudomonas chlororaphis]   | 1     | 79      | 59     |
| 412    | 1   | 1153   | 578  | gi 143177       | putative [Bacillus subtilis]  | 1     | 79      | 51     |
| 481    | 3   | 621    | 1124 | gi 786163       | Ribosomal Protein L10 [Bacillus subtilis]                                 | 1     | 79      | 66     |
| 516    | 1   | 702    | 352  | gi 805090       | NisF [Lactococcus lactis]   | 1     | 79      | 48     |
| 525    | 2   | 2457   | 1426 | gi 143371       | phosphoribosyl aminoimidazole synthetase (PUR-N) [Bacillus subtilis]      | 1     | 79      | 61     |
|        |     |        |      |                 | pir H29326 AB5CL phosphoribosylglycynamidine cyclo-ligase EC              | 1     | 1032    | 504    |
|        |     |        |      |                 | 6.3.3.1) - Bacillus subtilis  | 1     | 1       | 1      |
| 538    | 4   | 3448   | 2825 | gi 1370207      | lorf6 [Lactobacillus sake]  | 1     | 79      | 67     |
| 570    | 1   | 2      | 421  | gi 476160       | arginine permease substrate-binding subunit [Listeria monocytogenes]      | 1     | 79      | 61     |
| 645    | 8   | 2663   | 3241 | gi 153898       | transport protein [Salmonella typhimurium]                                | 1     | 79      | 62     |
| 683    | 1   | 75     | 374  | gi 1064795      | function unknown [Bacillus subtilis]                                      | 1     | 79      | 62     |
| 816    | 3   | 4700   | 3987 | gi 1407784      | orf-1; novel antigen [Staphylococcus aureus]                              | 1     | 79      | 62     |
| 2929   | 1   | 3      | 401  | gi 1524397      | glycine betaine transporter Opud [Bacillus subtilis]                      | 1     | 79      | 61     |
| 2937   | 1   | 357    | 202  | pir S52915 S529 | nitrate reductase alpha chain - Bacillus subtilis (fragment)              | 1     | 79      | 58     |
| 2940   | 1   | 768    | 385  | gi 149429       | putative [Lactococcus lactis]   | 1     | 79      | 72     |
| 2946   | 1   | 570    | 286  | gi 143267       | 12-oxoglutarate dehydrogenase (cdhA; EC 1.2.4.2) [Bacillus subtilis]      | 1     | 79      | 61     |
| 2999   | 1   | 3      | 212  | gi 710020       | nitrite reductase (nirB) [Bacillus subtilis]                              | 1     | 79      | 59     |
| 3022   | 1   | 514    | 332  | gi 450686       | 3-phosphoglycerate kinase [Thermotoga maritima]                           | 1     | 79      | 61     |
| 3064   | 1   | 3      | 314  | gi 1204436      | pyruvate formate-lyase [Haemophilus influenzae]                           | 1     | 79      | 60     |
| 3083   | 1   | 2      | 220  | gi 1149662      | hypD gene product [Clostridium perfringens]                               | 1     | 79      | 56     |
| 3126   | 1   | 701    | 411  | gi 1339950      | large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]  | 1     | 79      | 55     |
| 3181   | 1   | 607    | 326  | gi 1339950      | large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]  | 1     | 79      | 59     |
| 3345   | 1   | 3      | 476  | gi 871784       | Clp-like ATP-dependent protease binding subunit [Bos taurus]              | 1     | 79      | 63     |
| 3718   | 1   | 536    | 270  | pir C36889 C368 | lueB protein, inactive - Lactococcus lactis subsp. lactis (strain IL1403) | 1     | 79      | 71     |
| 3724   | 2   | 159    | 401  | gi 1009366      | Respiratory nitrate reductase [Bacillus subtilis]                         | 1     | 79      | 64     |
| 3836   | 1   | 608    | 312  | gi 1524193      | unknown [Mycobacterium tuberculosis]                                      | 1     | 79      | 65     |
| 3941   | 1   | 2      | 334  | gi 415855       | deoxyribose aldolase [Mycoplasma hominis]                                 | 1     | 79      | 54     |
| 4113   | 1   | 3      | 341  | gi 143015       | gluconate kinase [Bacillus subtilis]                                      | 1     | 79      | 63     |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop   | match      | match gene name  | % sim | % ident | length |
|--------|-----|--------|--------|------------|--|-------|---------|--------|
| ID     | ID  | (nt)   | (nt)   | accession  |  | (nt)  | (nt)    | (nt)   |
| 4501   | 1   | 406    | 209    | gi 1022726 | unknown [Staphylococcus haemolyticus]  | 79    | 66      | 198    |
| 4612   | 1   | 1      | 238    | gi 460689  | TVG [Thermoactinomyces vulgaris]   | 79    | 58      | 237    |
| 2      | 1   | 1      | 1213   | gi 520753  | DNA topoisomerase I [Bacillus subtilis]  | 78    | 64      | 1212   |
| 8      | 2   | 2266   | 1220   | gi 216151  | DNA polymerase (gene L; ttg start codon) [Bacteriophage SPO2] gi 579197  | 78    | 72      | 1047   |
|        |     |        |        |            | SP02 DNA polymerase (aa 1-648) [Bacteriophage SPO2] pir A214981 DJBPS2 DNA-<br>directed DNA polymerase (EC 2.7.7.7) - phage PC2  |       |         |        |
| 9      | 2   | 1340   | 1089   | gi 1064787 | function unknown [Bacillus subtilis]   | 78    | 57      | 252    |
| 32     | 8   | 6803   | 7702   | gi 146974  | [NH3-dependent NAD synthetase [Escherichia coli]   | 78    | 63      | 900    |
| 36     | 4   | 2941   | 3138   | gi 290503  | glutamate permease [Escherichia coli]  | 78    | 53      | 198    |
| 53     | 115 | 117684 | 16221  | gi 1303941 | YqIV [Bacillus subtilis]   | 78    | 58      | 1464   |
| 57     | 14  | 110520 | 112067 | gi 1072418 | lgIC gene product [Staphylococcus carnosus]  | 78    | 65      | 1548   |
| 66     | 7   | 6798   | 5812   | gi 1212729 | YqhJ [Bacillus subtilis]   | 78    | 67      | 987    |
| 67     | 4   | 4029   | 4376   | gi 466612  | InikA [Escherichia coli]   | 78    | 71      | 348    |
| 91     | 9   | 110058 | 110942 | gi 467380  | l stage 0 sporulation [Bacillus subtilis]  | 78    | 50      | 885    |
| 102    | 112 | 8574   | 110130 | gi 149426  | lputative [lactococcus lactis]   | 78    | 61      | 1557   |
| 112    | 6   | 3540   | 4463   | gi 854234  | lcymG gene product [Klebsiella oxytoca]  | 78    | 56      | 924    |
| 124    | 2   | 1888   | 11061  | gi 405622  | lunknown [Bacillus subtilis]   | 78    | 60      | 828    |
| 130    | 3   | 1805   | 2260   | gi 1256636 | lputative [Bacillus subtilis]  | 78    | 71      | 456    |
| 133    | 1   | 751    | 377    | gi 168060  | lAmB [Emericella nidulans]   | 78    | 59      | 375    |
| 166    | 4   | 7125   | 6163   | gi 451216  | lMannosephosphate Isomerase [Streptococcus mutans]   | 78    | 63      | 963    |
| 186    | 1   | 1586   | 1795   | gi 289284  | lcysteinyl-tRNA synthetase [Bacillus subtilis]   | 78    | 57      | 792    |
| 195    | 4   | 2749   | 2315   | gi 1353874 | lunknown [Rhodobacter capsulatus]  | 78    | 58      | 435    |
| 199    | 3   | 4279   | 3623   | gi 143525  | lsuccinate dehydrogenase cytochrome b-558 subunit [Bacillus subtilis]<br>pir A29843 DEBSSC succinate dehydrogenase (EC 1.3.99.1) cytochrome 558 -<br>Bacillus subtilis | 78    | 57      | 657    |
| 199    | 4   | 7209   | 5557   | gi 142521  | ldeoxyribodipyrimidine photolyase [Bacillus subtilis] pir A37192 A37192 uvrB<br>protein - Bacillus subtilis sp P14951 UVRC_BACSU EXCINUCLEASE ABC SUBUNIT<br>C.        | 78    | 62      | 1653   |
| 223    | 3   | 3831   | 3523   | gi 439596  | {Escherichia coli IS200 insertion sequence from ECOR63, partial., ene<br>product [Escherichia coli]}   | 78    | 47      | 309    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

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|--------|-----|-------|------|-----------------|--|-------|---------|--------|
| ID     | ID  | (nt)  | (nt) | accession       |  | (nt)  | (nt)    |        |
| 299    | 4   | 1865  | 2149 | gi 467439       | temperature sensitive cell division [Bacillus subtilis]  | 78    | 62      | 285    |
| 321    | 9   | 7734  | 7315 | gi 142979       | ORF3 is homologous to an ORF downstream of the spot gene of E.coli; RF3<br>[Bacillus stearothermophilus]   | 78    | 55      | 420    |
| 352    | 4   | 3714  | 3944 | gi 349050       | lactin 1 [Pneumocystis carinii]  | 78    | 42      | 231    |
| 352    | 5   | 7592  | 6093 | gi 903587       | [NADH dehydrogenase subunit 5 [Bacillus subtilis] sp P3975 NDHE_BACSU NADH<br>DEHYDROGENASE SUBUNIT 5 (EC 1.6.5.3) NADH-UBIQUINONE OXIDOREDUCTASE CHAIN<br>5]. | 78    | 58      | 1500   |
| 376    | 1   | 2     | 583  | gi 551693       | Idethiobiotin synthase [Bacillus sphaericus]   | 78    | 34      | 582    |
| 424    | 2   | 1595  | 1768 | gi 1524117      | alpha-acetolactate decarboxylase [Lactococcus lactis]  | 78    | 68      | 174    |
| 450    | 1   | 1914  | 988  | gi 1030068      | [NAD(P)H oxidoreductase, isoflavone reductase homologue [Solanum tuberosum]]   | 78    | 63      | 927    |
| 558    | 1   | 762   | 562  | gi 1511588      | bifunctional protein [Methanococcus jannaschii]  | 78    | 60      | 201    |
| 670    | 3   | 1152  | 1589 | gi 1122739      | Unknown [Bacillus subtilis]  | 78    | 64      | 438    |
| 714    | 1   | 64    | 732  | gi 143460       | [37 kd minor sigma factor (rpoF, sigB; ttg start codon) [Bacillus subtilis]]   | 78    | 57      | 669    |
| 814    | 1   | 3     | 368  | gi 1377833      | Unknown [Bacillus subtilis]  | 78    | 59      | 366    |
| 981    | 1   | 1381  | 692  | gi 143802       | GerC2 [Bacillus subtilis]  | 78    | 64      | 690    |
| 995    | 2   | 978   | 727  | gi 296947       | luridine kinase [Escherichia coli]   | 78    | 64      | 252    |
| 1045   | 1   | 3     | 401  | gi 1407784      | lorf-1; novel antigen [Staphylococcus aureus]  | 78    | 61      | 399    |
| 1163   | 2   | 368   | 186  | gi 410117       | [diaminopimelate decarboxylase [Bacillus subtilis]]  | 78    | 54      | 183    |
| 2191   | 1   | 794   | 399  | gi 215098       | excisionase [Bacteriophage 154a]   | 78    | 65      | 396    |
| 2933   | 1   | 2     | 181  | gi 1204436      | pyruvate formate-lyase [Haemophilus influenzae]  | 78    | 73      | 180    |
| 3041   | 2   | 129   | 317  | gi 624632       | lGltL [Escherichia coli]   | 78    | 53      | 189    |
| 3581   | 1   | 105   | 401  | gi 763186       | [3-ketoacyl-coA thiolase [Saccharomyces cerevisiae]]   | 78    | 55      | 297    |
| 3709   | 1   | 3     | 230  | gi 460689       | TVG [Thermoactinomyces vulgaris]   | 78    | 58      | 228    |
| 3974   | 1   | 528   | 265  | gi 558839       | Unknown [Bacillus subtilis]  | 78    | 65      | 264    |
| 3980   | 1   | 3     | 401  | gi 39956        | lIGlc [Bacillus subtilis]  | 78    | 62      | 399    |
| 4056   | 1   | 647   | 354  | gi 1256635      | dihydroxy-acid dehydratase [Bacillus subtilis]   | 78    | 55      | 294    |
| 4114   | 1   | 630   | 316  | pir S09372 S093 | [hypothetical protein - Trypanosoma brucei]  | 78    | 62      | 315    |
| 4185   | 1   | 3     | 179  | gi 1339950      | large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]   | 78    | 58      | 177    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop  | match<br>ID | match<br>(nt) | match<br>accession | match<br>gene name   | % sim | % ident | length<br>(nt) |
|--------|-----|-------|-------|-------------|---------------|--------------------|--|-------|---------|----------------|
| 4235   | 1   | 655   | 329   | gi 558839   | gi 603768     | gi 1353678         | Unknown [Bacillus subtilis]  | 78    | 60      | 327            |
| 4352   | 1   | 541   | 302   | gi 603768   | gi 1353678    | gi 603768          | HutI protein, imidazolone-5-propionate hydrolase [Bacillus subtilis]         | 78    | 63      | 240            |
| 4368   | 1   | 612   | 307   | gi 1353678  | gi 1276841    | gi 1276841         | imidazolone-5-propionate hydrolase [Bacillus subtilis]                       | 78    | 59      | 306            |
| 4461   | 1   | 428   | 216   | gi 1276841  | gi 39956      | gi 39956           | heavy-metal transporting P-type ATPase [Proteus mirabilis]                   | 78    | 36      | 213            |
| 4530   | 1   | 474   | 238   | gi 39956    | gi 1109684    | gi 1109684         | glutamate synthase (GOGAT) [Pophyra purpurea]                                | 78    | 65      | 237            |
| 3      | 2   | 2969  | 2073  | gi 1109684  | gi 1212728    | gi 1212728         | ribosomal protein L9 [Bacillus subtilis]                                     | 77    | 56      | 897            |
| 12     | 2   | 2426  | 1965  | gi 467335   | gi 1212728    | gi 1212728         | ribosomal protein L9 [Bacillus subtilis]                                     | 77    | 59      | 462            |
| 27     | 1   | 2     | 388   | gi 40054    | gi 1212728    | gi 1212728         | ribosomal protein L9 [Bacillus subtilis]                                     | 77    | 63      | 387            |
| 39     | 2   | 590   | 1252  | gi 40054    | gi 606241     | gi 606241          | phenylalanyl-tRNA synthetase beta subunit (AA 1-804) [Bacillus subtilis]     | 77    | 60      | 663            |
| 42     | 6   | 2704  | 2931  | gi 606241   | gi 1297798    | gi 1297798         | 30S ribosomal subunit protein S14 [Escherichia coli] sp P02370 RS14_ECOLI    | 77    | 65      | 228            |
| 46     | 18  | 15459 | 16622 | gi 1297798  | gi 1297798    | gi 1297798         | 30S RIBOSOMAL PROTEIN S14. (SUB 2101)  | 77    | 55      | 1164           |
| 100    | 4   | 4562  | 4002  | gi 1340128  | gi 1340128    | gi 1340128         | mitochondrial formate dehydrogenase precursor [Solanum tuberosum]            | 77    | 54      | 561            |
| 102    | 8   | 5378  | 5713  | gi 1311482  | gi 1237015    | gi 1237015         | pir JQ2272 JQ2272 formate dehydrogenase (EC 1.2.1.2) precursor,              | 77    | 57      | 336            |
| 109    | 7   | 4742  | 5383  | gi 710637   | gi 710637     | gi 710637          | mitochondrial - potato   | 77    | 56      | 642            |
| 117    | 1   | 2     | 1228  | gi 1237015  | gi 1237015    | gi 1237015         | pir JQ2272 JQ2272 formate dehydrogenase (EC 1.2.1.2) precursor,              | 77    | 53      | 1227           |
| 124    | 10  | 8323  | 7688  | gi 405819   | gi 405819     | gi 405819          | acetolactate synthase [Thermus aquaticus]                                    | 77    | 63      | 636            |
| 147    | 3   | 1146  | 985   | gi 849027   | gi 849027     | gi 849027          | thymidine kinase [Bacillus subtilis]   | 77    | 37      | 162            |
| 152    | 10  | 7354  | 7953  | gi 1205583  | gi 1205583    | gi 1205583         | hypothetical 15.9-kDa protein [Bacillus subtilis]                            | 77    | 55      | 600            |
| 169    | 2   | 1004  | 1282  | gi 473825   | gi 473825     | gi 473825          | spermidine/putrescine transport ATP-binding protein [Haemophilus influenzae] | 77    | 58      | 279            |
| 184    | 2   | 380   | 1147  | gi 216314   | gi 216314     | gi 216314          | 'elongation factor EF-Ts' [Escherichia coli]                                 | 77    | 60      | 768            |
| 189    | 7   | 3296  | 3868  | gi 853809   | gi 853809     | gi 853809          | esterase [Bacillus stearothermophilus]                                       | 77    | 48      | 573            |
| 193    | 1   | 132   | 290   | gi 1303788  | gi 1303788    | gi 1303788         | ORF3 [Clostridium perfringens]   | 77    | 54      | 159            |
| 195    | 8   | 8740  | 8414  | gi 1499620  | gi 1499620    | gi 1499620         | M. jannaschii predicted coding region MJ0798 [Methanococcus jannaschii]      | 77    | 44      | 327            |
| 205    | 8   | 5428  | 5204  | gi 216340   | gi 216340     | gi 216340          | ORF for adenylylate kinase [Bacillus subtilis]                               | 77    | 61      | 225            |

## S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop  | match           | match gene name   | % sim | % ident | length |
|--------|-----|-------|-------|-----------------|---|-------|---------|--------|
| ID     | ID  | (nt)  | (nt)  | accession       |   | (nt)  |         | (nt)   |
| 205    | 129 | 14795 | 14502 | gi 786155       | Ribosomal Protein L23 [Bacillus subtilis]                                   | 1     | 77      | 62     |
| 211    | 5   | 1908  | 2084  | gi 410132       | ORFX8 [Bacillus subtilis]   | 1     | 77      | 47     |
| 217    | 5   | 3478  | 4416  | gi 496254       | fibronectin/fibrinogen-binding protein [Streptococcus pyogenes]             | 1     | 77      | 54     |
| 232    | 1   | 267   | 998   | gi 1407784      | orf-1; novel antigen [Staphylococcus aureus]                                | 1     | 77      | 57     |
| 233    | 2   | 1819  | 1346  | gi 467408       | unknown [Bacillus subtilis]   | 1     | 77      | 61     |
| 243    | 3   | 2661  | 2299  | gi 516155       | unconventional myosin [Sus scrofa]  | 1     | 77      | 32     |
| 299    | 1   | 68    | 769   | gi 467436       | unknown [Bacillus subtilis]   | 1     | 77      | 54     |
| 301    | 4   | 1468  | 1283  | gi 950071       | ATP-bind. pyrimidine kinase [Mycoplasma capricolum] pir S48605 S48605       | 1     | 77      | 48     |
| 302    | 5   | 2741  | 3211  | gi 508980       | hypothetical protein - Mycoplasma capricolum SEC3 (fragment)                | 1     | 77      | 1      |
| 302    | 7   | 3835  | 4863  | gi 147783       | lruvB protein [Escherichia coli]  | 1     | 77      | 60     |
| 307    | 9   | 5402  | 4797  | gi 1070015      | lprotein-dependent [Bacillus subtilis]                                      | 1     | 77      | 60     |
| 312    | 1   | 99    | 1391  | gi 143165       | lmalic enzyme (EC 1.1.1.38) [Bacillus stearothermophilus] pir A33307 DEBSXS | 1     | 77      | 62     |
| 312    | 2   | 1541  | 2443  | gi 1399855      | lmalic enzyme (EC 1.1.1.38) [Bacillus stearothermophilus] pir A33307 DEBSXS | 1     | 77      | 58     |
| 321    | 5   | 5666  | 4596  | gi 39844        | lmalate dehydrogenase oxaloacetate-decarboxylating (EC 1.1.1.38) -          | 1     | 77      | 1      |
| 354    | 1   | 47    | 568   | gi 1154634      | Bacillus stearothermophilus   | 1     | 77      | 57     |
| 365    | 1   | 2     | 1021  | gi 143374       | lYmaB [Bacillus subtilis]   | 1     | 77      | 62     |
| 374    | 1   | 1     | 708   | gi 1405446      | ltransketolase [Bacillus subtilis]  | 1     | 77      | 61     |
| 385    | 1   | 1128  | 565   | gi 533099       | lendonuclease III [Bacillus subtilis]                                       | 1     | 77      | 63     |
| 392    | 2   | 594   | 1940  | gi 556014       | lUDP-N-acetyl muramate-alanine ligase [Bacillus subtilis]                   | 1     | 77      | 65     |
| 405    | 5   | 4079  | 3570  | gi 1303912      | sp P40778 MURC UDP-N-ACETYL MURAMATE--ALANINE LIGASE (EC .3.2.8.)           | 1     | 77      | 1      |
| 487    | 4   | 1302  | 1472  | gi 432427       | (UDP-N- ACETYL MURANOYL-L-ALANINE SYNTHETASE) (FRAGMENT)                    | 1     | 77      | 48     |
| 522    | 1   | 2     | 562   | pir A01179 SYBS | lORF1 gene product [Acinetobacter calcoaceticus]                            | 1     | 77      | 1      |
|        |     |       |       |                 | Bacillus stearothermophilus   | 1     | 77      | 561    |

## S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF ID | Start (nt) | Stop (nt) | match accession | match gene name   | % sim | % ident | length (nt) |
|--------|--------|------------|-----------|-----------------|---|-------|---------|-------------|
| 523    | 2      | 1587       | 1351      | gi 1387979      | 44% identity over 302 residues with hypothetical protein from Synechocystis sp., accession D64006 CD; expression induced by environmental stress; some similarity to glycosyl transferases; two potential membrane-spanning helices [Bacillus subtilis] | 77    | 48      | 237         |
| 536    | 2      | 983        | 612       | gi 143366       | adenylosuccinate lyase (PUR-B) [Bacillus subtilis] pir C29326 WZB5DS  | 77    | 61      | 372         |
| 548    | 2      | 339        | 872       | gi 143387       | adenylosuccinate lyase (EC 4.3.2.2) - Bacillus subtilis   | 77    | 56      | 534         |
| 597    | 1      | 2          | 481       | gi 904198       | aspartate transcarbamylase [Bacillus subtilis]  | 77    | 33      | 480         |
| 633    | 1      | 1747       | 1313      | gi 387577       | hypothetical protein [Bacillus subtilis]  | 77    | 64      | 435         |
| 642    | 1      | 85         | 360       | gi 46971        | ORFLA [Bacillus subtilis]   | 77    | 61      | 276         |
| 659    | 1      | 125        | 1219      | gi 1072381      | epiP gene product [Staphylococcus epidermidis]  | 77    | 62      | 1095        |
| 670    | 4      | 1587       | 1820      | gi 1122760      | glutamyl-aminopeptidase [Lactococcus lactis]  | 77    | 58      | 234         |
| 789    | 1      | 2          | 391       | gi 1377823      | laminopeptidase [Bacillus subtilis]   | 77    | 65      | 390         |
| 815    | 1      | 10         | 573       | gi 1303861      | unknown [Bacillus subtilis]   | 77    | 49      | 564         |
| 899    | 1      | 1          | 225       | gi 1204844      | YggN [Bacillus subtilis]  | 77    | 55      | 225         |
| 1083   | 1      | 3          | 188       | gi 460828       | predicted coding region HI0594 [Haemophilus influenzae]   | 77    | 66      | 186         |
| 1942   | 1      | 415        | 209       | gi 160047       | basic repeat antigen [Plasmodium falciparum] pir A2932 A29232   | 77    | 38      | 207         |
| 2559   | 1      | 1          | 171       | gi 1499034      | 101K malaria antigen precursor - Plasmodium alciparum (strain Camp)   | 77    | 61      | 171         |
| 2933   | 2      | 243        | 401       | gi 42370        | M. jannaschii predicted coding region MJ0255 [Methanococcus jannaschii]   | 77    | 72      | 159         |
| 2966   | 1      | 56         | 292       | gi 1524397      | pyruvate formate-lyase (AA 1-760) [Escherichia coli] ir S01788 S01788   | 77    | 45      | 237         |
| 2976   | 1      | 614        | 309       | gi 40003        | formate C-acetyltransferase (EC 2.3.1.54) - cherichia coli  | 77    | 60      | 306         |
| 2979   | 2      | 678        | 400       | gi 1204354      | glycine betaine transporter OpnD [Bacillus subtilis]  | 77    | 61      | 279         |
| 2988   | 1      | 601        | 377       | gi 438465       | 2-OXOGLUTARATE DEHYDROGENASE EI COMPONENT (EC 2.4.2) (ALPHA- KETOGULUTARATE DEHYDROGENASE).   | 77    | 55      | 225         |
| 2990   | 1      | 331        | 167       | gi 142562       | Probable operon with orff. Possible alternative initiation codon, ases 2151-2153. Homology with acetyltransferases.; putative Bacillus subtilis]  | 77    | 63      | 165         |
| 3032   | 1      | 3          | 389       | gi 488430       | ATP synthase epsilon subunit [Bacillus megaterium] pir B28599 PB8599 H+ transporting ATP synthase (EC 3.6.1.34) psilon chain - Bacillus megaterium  | 77    | 56      | 387         |
| 3057   | 1      | 1          | 195       | gi 468764       | alcohol dehydrogenase 2 [Entamoeba histolytica]   | 77    | 50      | 195         |
|        |        |            |           |                 | lmoCR gene product [Rhizobium meliloti]   |       |         |             |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop   | match<br>accession | match<br>gene name  | % sim | % ident | length<br>(nt) |
|--------|-----|--------|--------|--------------------|---|-------|---------|----------------|
| ID     | ID  | (nt)   | (nt)   |                    |   |       |         |                |
| 4008   | 1   | 726    | 400    | gi 603768          | HutI protein, imidazolone-5-propionate hydrolase [Bacillus subtilis]<br>gi 603768 HutI protein, imidazolone-5-propionate hydrolase Bacillus subtilis  | 77    | 52      | 327            |
| 4048   | 1   | 703    | 386    | gi 216278          | lgramicidin S synthetase 1 [Bacillus brevis]  | 77    | 55      | 318            |
| 4110   | 1   | 3      | 368    | ipr S52915 S529    | Intrate reductase alpha chain - Bacillus subtilis (fragment)  | 77    | 61      | 366            |
| 4115   | 1   | 1      | 348    | gi 517205          | 167 kDa Myosin-crossreactive streptococcal antigen [Streptococcus yogenes]  | 77    | 65      | 348            |
| 4225   | 1   | 590    | 297    | gi 1322245         | lmevalonate pyrophosphate decarboxylase [Rattus norvegicus]   | 77    | 60      | 294            |
| 4611   | 2   | 494    | 327    | gi 508979          | GTP-binding protein [Bacillus subtilis]   | 77    | 57      | 168            |
| 4668   | 1   | 361    | 182    | ipr S52915 S529    | Intrate reductase alpha chain - Bacillus subtilis (fragment)  | 77    | 61      | 180            |
| 25     | 1   | 2      | 1627   | gi 1150620         | MmsA [Streptococcus pneumoniae]   | 76    | 58      | 1626           |
| 38     | 5   | 1488   | 2537   | ipr A43577 A435    | regulatory protein pf0R - Clostridium perfringens   | 76    | 57      | 1050           |
| 52     | 5   | 2962   | 4041   | gi 1161061         | ldioxygenase [Methylobacterium extorquens]  | 76    | 62      | 1080           |
| 56     | 120 | 127389 | 127955 | gi 467402          | lunknown [Bacillus subtilis]  | 76    | 56      | 567            |
| 57     | 15  | 112046 | 112219 | gi 1206040         | lweak similarity to keratin [Caenorhabditis elegans]  | 76    | 40      | 174            |
| 91     | 2   | 1062   | 2261   | gi 475715          | lacetyl coenzyme A acetyltransferase (thiolase) [Clostridium acetobutylicum]  | 76    | 57      | 1200           |
| 98     | 2   | 818    | 1624   | gi 467422          | lunknown [Bacillus subtilis]  | 76    | 62      | 807            |
| 98     | 5   | 2965   | 3228   | gi 897793          | ly98 gene product [Pediococcus acidilactici]  | 76    | 52      | 264            |
| 98     | 8   | 5922   | 6326   | gi 467427          | lmethionyl-tRNA synthetase [Bacillus subtilis]  | 76    | 53      | 405            |
| 104    | 3   | 1322   | 1885   | gi 216151          | lDNA polymerase (gene L; ttg start codon) [Bacteriophage SPO2] gi 579197<br>SP02 DNA polymerase (aa 1-648) [Bacteriophage SPO2] piri A21498 DJBPS2 DNA-<br>directed DNA polymerase (EC 2.7.7) - phage P02 | 76    | 63      | 564            |
| 124    | 9   | 8134   | 7055   | gi 853776          | lpeptide chain release factor 1 [Bacillus subtilis] piri S55437 S55437<br>lpeptide chain release factor 1 - Bacillus subtilis   | 76    | 58      | 1080           |
| 164    | 5   | 2832   | 3311   | gi 1204976         | lprolyl-tRNA synthetase [Haemophilus influenzae]  | 76    | 53      | 480            |
| 168    | 2   | 2617   | 1841   | gi 1177253         | lputative ATP-binding protein of ABC-type [Bacillus subtilis]   | 76    | 58      | 777            |
| 189    | 2   | 163    | 888    | gi 467384          | lunknown [Bacillus subtilis]  | 76    | 63      | 726            |
| 235    | 3   | 2253   | 3518   | gi 142936          | lfatty polyglutamate synthetase [Bacillus subtilis] piri B40646 B40646 folC -<br>Bacillus subtilis  | 76    | 53      | 1266           |
| 236    | 1   | 335    | 925    | gi 1146197         | lputative [Bacillus subtilis]   | 76    | 54      | 591            |
| 237    | 8   | 5323   | 5541   | gi 1279261         | lF13G3.6 [Caenorhabditis elegans]   | 76    | 47      | 219            |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop | match      | match gene name   | % sim | % ident | length |
|--------|-----|-------|------|------------|---|-------|---------|--------|
| ID     | ID  | (nt)  | (nt) | accession  |   | (nt)  | (nt)    | (nt)   |
| 263    | 5   | 5490  | 4585 | gi 1510348 | l dihydriodicolinate synthase [Methanococcus jannaschii]                                    | 76    | 49      | 906    |
| 304    | 3   | 1051  | 1794 | gi 666982  | putative membrane spanning subunit [Bacillus subtilis] Pir SS52382 SS52382                  | 76    | 60      | 744    |
|        |     |       |      |            | probable membrane spanning protein - Bacillus subtilis                                      |       |         |        |
| 312    | 4   | 3611  | 4624 | gi 143312  | 6-phospho-1-fructokinase (gtg start codon; EC 2.7.1.11) [Bacillus tearothermophilus]        | 76    | 56      | 1014   |
| 343    | 1   | 2     | 1036 | gi 405956  | lyeeE [Escherichia coli]  | 76    | 59      | 1035   |
| 347    | 1   | 409   | 1701 | gi 396304  | l acetylornithine deacetylase [Escherichia coli]  | 76    | 72      | 1293   |
| 358    | 1   | 672   | 1907 | gi 1146215 | l 39.0% identity to the Escherichia coli S1 ribosomal protein; putative [Bacillus subtilis] | 76    | 58      | 1236   |
| 371    | 1   | 1     | 222  | gi 537084  | l alternate gene name mgt; CG Site No. 497 [Escherichia coli]                               | 76    | 61      | 222    |
|        |     |       |      |            | Pir SS56468 SS56468 mgtA protein - Escherichia coli   |       |         |        |
| 379    | 4   | 4331  | 4858 | gi 143268  | l dihydrolipoamide transsuccinylase (odhB; EC 2.3.1.61) [Bacillus subtilis]                 | 76    | 61      | 528    |
| 404    | 5   | 4022  | 4492 | gi 1303823 | l YqfG [Bacillus subtilis]  | 76    | 60      | 471    |
| 411    | 1   | 2     | 307  | gi 486025  | l ORF YKL027w [Saccharomyces cerevisiae]  | 76    | 55      | 306    |
| 472    | 3   | 4356  | 2854 | gi 1405464 | l Alst [Bacillus subtilis]  | 76    | 57      | 1503   |
| 546    | 1   | 273   | 995  | gi 153821  | l streptococcal pyrogenic exotoxin type C (speC) precursor [Streptococcus pyogenes]         | 76    | 36      | 723    |
| 588    | 1   | 1054  | 557  | gi 1002520 | l MutS [Bacillus subtilis]  | 76    | 61      | 498    |
| 591    | 1   | 16    | 735  | gi 885934  | l ClpB [Synechococcus sp.]  | 76    | 44      | 720    |
| 602    | 2   | 175   | 798  | gi 1486422 | l OppD homologue [Rhizobium sp.]  | 76    | 52      | 624    |
| 619    | 2   | 547   | 290  | gi 330613  | l major capsid protein [Human cytomegalovirus]  | 76    | 47      | 258    |
| 660    | 4   | 2568  | 3302 | gi 904199  | l hypothetical protein [Bacillus subtilis]  | 76    | 55      | 735    |
| 677    | 1   | 452   | 228  | gi 40177   | l spoOF gene product [Bacillus subtilis]  | 76    | 58      | 225    |
| 962    | 1   | 24    | 206  | gi 142443  | l adenylosuccinate synthetase [Bacillus subtilis] sp P29726 PURA_BACSU                      | 76    | 67      | 183    |
|        |     |       |      |            | ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) IMP--ASPARTATE LIGASE.                             |       |         |        |
| 978    | 1   | 1158  | 580  | gi 1511333 | l M. jannaschii predicted coding region MJ1322 [Methanococcus jannaschii]                   | 76    | 56      | 579    |
| 997    | 1   | 486   | 244  | gi 467154  | l No definition line found [Mycobacterium leprae]   | 76    | 38      | 243    |
|        |     |       |      |            |   |       |         |        |
| 1563   | 1   | 529   | 266  | gi 1303984 | l YqkG [Bacillus subtilis]  | 76    | 52      | 264    |
| 2184   | 1   | 361   | 182  | gi 506706  | l CapJ [Staphylococcus aureus]  | 76    | 38      | 180    |
| 2572   | 1   | 1     | 387  | gi 153898  | l transport protein [Salmonella typhimurium]  | 76    | 65      | 387    |

## S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop   | match          | gene name  | % sim | % ident | length |
|--------|-----|--------|--------|----------------|--|-------|---------|--------|
| ID     | ID  | (nt)   | (nt)   | accession      |  | (nt)  | (nt)    |        |
| 2942   | 1   | 29     | 400    | gi 710020      | linitrite reductase (nirB) [Bacillus subtilis]                               | 76    | 59      | 372    |
| 2957   | 1   | 377    | 216    | gi 1511251     | hypothesetical protein (SP:PI2404) [Methanococcus jannaschii]                | 76    | 47      | 162    |
| 2980   | 1   | 554    | 279    | gi 1405464     | Alst [Bacillus subtilis]   | 76    | 53      | 276    |
| 3015   | 1   | 649    | 326    | gi 408115      | lornithine acetyltransferase [Bacillus subtilis]                             | 76    | 61      | 324    |
| 3124   | 1   | 13     | 174    | gi 882705      | ORF_0401 [Escherichia coli]  | 76    | 65      | 162    |
| 3179   | 1   | 3      | 161    | gi 168477      | ferredoxin-dependent glutamate synthase [Zea mays] pir A38596 A38596         | 76    | 53      | 159    |
|        |     |        |        |                | l glutamate synthase (ferredoxin) (EC 1.4.7.1) - aize                        |       |         |        |
| 3789   | 1   | 2      | 379    | gi 39956       | lIGlc [Bacillus subtilis]  | 76    | 55      | 378    |
| 3892   | 1   | 3      | 314    | gi 1510398     | lerripyochelin binding protein [Methanococcus jannaschii]                    | 76    | 52      | 312    |
| 3928   | 1   | 798    | 400    | gi 143016      | lpermease [Bacillus subtilis]  | 76    | 59      | 399    |
| 4159   | 1   | 757    | 386    | sp P80544 MRSP | lMETHICILLIN-RESISTANT SURFACE PROTEIN (FRAGMENTS).                          | 76    | 66      | 372    |
| 4204   | 1   | 17     | 331    | gi 296464      | lATPase [Lactococcus lactis]   | 76    | 56      | 315    |
| 4398   | 1   | 494    | 249    | gi 987255      | lMenkes disease gene [Homo sapiens]  | 76    | 48      | 246    |
| 4506   | 1   | 2      | 313    | gi 216746      | lD-lactate dehydrogenase [Lactobacillus plantarum]                           | 76    | 47      | 312    |
| 4546   | 1   | 477    | 247    | gi 1339950     | lLarge subunit of NADH-dependent glutamate synthase [Plectonema boryanum]    | 76    | 61      | 231    |
| 4596   | 1   | 379    | 191    | gi 560027      | lcellulose synthase [Acetobacter xylinum]                                    | 76    | 70      | 189    |
| 4      | 5   | 5257   | 4337   | gi 882532      | lORF_0294 [Escherichia coli]   | 75    | 59      | 921    |
| 6      | 1   | 164    | 952    | gi 40960       | lOTCase [Escherichia coli]   | 75    | 56      | 789    |
| 12     | 3   | 5935   | 3944   | gi 467336      | lUnknown [Bacillus subtilis]   | 75    | 57      | 1992   |
| 23     | 18  | 18272  | 17310  | gi 1296433     | lO-acetylserine sulfhydrylase B [Alcaligenes eutrophus]                      | 75    | 55      | 963    |
| 25     | 3   | 2356   | 3393   | gi 1502419     | lPLX [Bacillus subtilis]   | 75    | 56      | 1038   |
| 36     | 8   | 5765   | 6037   | gi 1256517     | lUnknown [Schizosaccharomyces pombe]   | 75    | 45      | 273    |
| 46     | 13  | 111186 | 112058 | gi 48972       | lNitrate transporter [Synechococcus sp.]                                     | 75    | 46      | 873    |
| 51     | 7   | 3474   | 3677   | gi 143607      | lSporulation protein [Bacillus subtilis]                                     | 75    | 61      | 204    |
| 53     | 16  | 116850 | 116590 | gi 143402      | lrecombination protein (ttg start codon) [Bacillus subtilis] gi 1303923 RecN | 75    | 51      | 261    |
|        |     |        |        |                | l [Bacillus subtilis]  |       |         |        |
| 74     | 3   | 3572   | 2568   | gi 1204847     | lornithine carbamoyltransferase [Haemophilus influenzae]                     | 75    | 61      | 1005   |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop  | match          | match gene name   | % sim | % ident | length |
|--------|-----|-------|-------|----------------|---|-------|---------|--------|
| ID     | ID  | (nt)  | (nt)  | accession      |   |       |         | (nt)   |
| 85     | 3   | 4628  | 3930  | gi 143368      | phosphoribosyl glycaminidine synthetase I (PUR-L; gtg start odon)           | 75    | 63      | 699    |
| 85     | 5   | 5588  | 4878  | gi 143367      | phosphoribosyl aminodazole succinocarboxamide synthetase (PUR-C; tg start   | 75    | 55      | 711    |
| 85     | 8   | 6625  | 7530  | gi 1303916     | codon) [Bacillus subtilis]  | 75    | 53      | 906    |
| 87     | 3   | 2340  | 3590  | gi 1064813     | homologous to sp:PHOR_BACSU [Bacillus subtilis]                             | 75    | 56      | 1251   |
| 87     | 6   | 6084  | 6896  | gi 1064810     | function unknown [Bacillus subtilis]  | 75    | 61      | 813    |
| 108    | 2   | 1844  | 1503  | gi 1001824     | hypothetical protein [Synechocystis sp.]                                    | 75    | 51      | 342    |
| 110    | 3   | 1748  | 3727  | gi 1147593     | putative ppGpp synthetase [Streptomyces coelicolor]                         | 75    | 55      | 1980   |
| 110    | 7   | 4353  | 5252  | gi 1177251     | clwD gene product [Bacillus subtilis]                                       | 75    | 75      | 900    |
| 120    | 14  | 11266 | 10649 | gi 1524394     | ORF-2 upstream of gbsAB operon [Bacillus subtilis]                          | 75    | 55      | 618    |
| 121    | 5   | 2050  | 4221  | gi 1154632     | NRDE [Bacillus subtilis]  | 75    | 54      | 2172   |
| 124    | 1   | 283   | 143   | gi 405622      | unknown [Bacillus subtilis]   | 75    | 56      | 141    |
| 128    | 1   | 81    | 1139  | gi 143316      | [gap] gene products [Bacillus megaterium]                                   | 75    | 48      | 1059   |
| 130    | 8   | 5760  | 5903  | gi 1256654     | 54.8% identity with Neisseria gonorrhoeae regulatory protein PilB; putative | 75    | 62      | 144    |
| 136    | 2   | 4480  | 3185  | gi 467403      | seryl-tRNA synthetase [Bacillus subtilis]                                   | 75    | 54      | 1296   |
| 161    | 10  | 5439  | 5798  | gi 1001195     | hypothetical protein [Synechocystis sp.]                                    | 75    | 55      | 360    |
| 172    | 4   | 3819  | 2995  | gi 755153      | ATP-binding protein [Bacillus subtilis]                                     | 75    | 52      | 825    |
| 179    | 1   | 2024  | 1107  | gi 143037      | porphobilinogen deaminase [Bacillus subtilis]                               | 75    | 58      | 918    |
| 195    | 10  | 9529  | 9374  | sp P25745 YCFB | HYPOTHETICAL PROTEIN IN PURB 5' REGION (FRAGMENT).                          | 75    | 60      | 156    |
| 200    | 4   | 2605  | 4596  | gi 142440      | ATP-dependent nuclelease [Bacillus subtilis]                                | 75    | 56      | 1992   |
| 206    | 3   | 6900  | 5620  | gi 1256135     | YbbF [Bacillus subtilis]  | 75    | 53      | 1281   |
| 216    | 2   | 159   | 389   | gi 1052800     | unknown [Schizosaccharomyces pombe]   | 75    | 58      | 231    |
| 229    | 1   | 29    | 847   | gi 1205958     | branched chain aa transport system II carrier protein [Haemophilus          | 75    | 49      | 819    |
| 230    | 2   | 518   | 1714  | gi 971337      | nitrite extrusion protein [Bacillus subtilis]                               | 75    | 53      | 1197   |
| 231    | 1   | 2240  | 1122  | gi 1002521     | MutL [Bacillus subtilis]  | 75    | 54      | 1119   |
| 233    | 3   | 1314  | 1859  | gi 467405      | unknown [Bacillus subtilis]   | 75    | 59      | 546    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop | match            | match gene name  | % sim | % ident | length |
|--------|-----|-------|------|------------------|--|-------|---------|--------|
| ID     | ID  | (nt)  | (nt) | accession        |  |       |         | (nt)   |
| 269    | 1   | 325   | 164  | lgi 1511246      | methyl coenzyme M reductase system, component A2 [Methanococcus jannaschii]  | 75    | 50      | 162    |
| 292    | 1   | 1389  | 772  | lgi 1511604      | M. jannaschii predicted coding region MJ1651 [Methanococcus jannaschii]  | 75    | 46      | 618    |
| 304    | 4   | 1773  | 2261 | lgi 1205328      | surfactin [Haemophilus influenzae]   | 75    | 55      | 489    |
| 312    | 3   | 2437  | 3387 | lgi 285621       | undefined open reading frame [Bacillus stearothermophilus]   | 75    | 62      | 951    |
| 312    | 5   | 4622  | 6403 | lgi 1041097      | Pyruvate Kinase [Bacillus psychrophilus]   | 75    | 57      | 1782   |
| 319    | 1   | 353   | 877  | lgi 1212728      | Yqhi [Bacillus subtilis]   | 75    | 54      | 525    |
| 320    | 5   | 4321  | 5031 | lgi 1070361      | OMP decarboxylase [Lactococcus lactis]   | 75    | 56      | 711    |
| 320    | 6   | 5010  | 5642 | lgi 143394       | OMP-PRPP transferase [Bacillus subtilis]   | 75    | 60      | 633    |
| 337    | 4   | 1519  | 2088 | lgi 487433       | citrate synthase II [Bacillus subtilis]  | 75    | 58      | 570    |
| 394    | 2   | 669   | 1271 | lgi 304976       | matches PS00017: ATP_GTP_A and PS00301: EFACTOR_GTP; similar to elongation factor G, TetM/TetO_tetracycline-resistance proteins Escherichia coli   | 75    | 51      | 603    |
| 423    | 1   | 127   | 570  | lgi 1183839      | unknown [Pseudomonas aeruginosa]   | 75    | 59      | 444    |
| 433    | 2   | 1603  | 1929 | lgi 149211       | acetolactate synthase [Klebsiella pneumoniae]  | 75    | 63      | 327    |
| 446    | 2   | 176   | 1540 | lgi 312441       | dihydroorotate [Bacillus caldolyticus]   | 75    | 62      | 1365   |
| 486    | 1   | 494   | 249  | lgi 1149682      | lptotF gene product [Clostridium perfringens]  | 75    | 55      | 246    |
| 496    | 1   | 3     | 794  | lgi 143582       | lspolIIIEA protein [Bacillus subtilis]   | 75    | 59      | 792    |
| 498    | 2   | 824   | 1504 | lgi 143328       | lphoP protein (put.); putative [Bacillus subtilis]   | 75    | 47      | 681    |
| 499    | 2   | 1061  | 1624 | lgi 1387979      | 448 identity over 302 residues with hypothetical protein from Synechocystis sp, accession D64006_CD; expression induced by environmental stress; some similarity to glycosyl transferases; two potential membrane-spanning helices (Bacillus subtilis) | 75    | 51      | 564    |
| 568    | 1   | 641   | 453  | lpir JC4110 JC41 | triaacylglycerol lipase (EC 3.1.1.3) 2 - Mycoplasma mycoides subsp. mycoides   | 75    | 50      | 189    |
| 613    | 2   | 430   | 233  | lgi 330993       | tegument protein [Saimiriine herpesvirus 2]  | 75    | 75      | 198    |
| 621    | 1   | 1     | 525  | lgi 529754       | lspc [Streptococcus pyogenes]  | 75    | 43      | 525    |
| 642    | 5   | 1809  | 2474 | lgi 1176401      | EpiG [Staphylococcus epidermidis]  | 75    | 51      | 666    |
| 646    | 2   | 454   | 657  | lgi 172442       | ribonuclease P [Saccharomyces cerevisiae]  | 75    | 37      | 204    |
| 657    | 1   | 3     | 347  | lgi 882541       | ORF_o236 [Escherichia coli]  | 75    | 47      | 345    |
| 750    | 1   | 1662  | 832  | lgi 46971        | lepiP gene product [Staphylococcus epidermidis]  | 75    | 57      | 831    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop | match     | gene name  | % sim   | % ident | length |
|--------|-----|-------|------|-----------|--|---|---------|--------|
| ID     | ID  | (nt)  | (nt) | accession |  | (nt)  |         | (nt)   |
| 754    | 1   | 1     | 2    | 481       | gi 1303901   | Yqht [Bacillus subtilis]  | 75      | 57     |
| 763    | 1   | 2     | 563  | 393       | gi 1205145   | Multidrug resistance protein [Haemophilus influenzae]                       | 75      | 51     |
| 775    | 1   | 1     | 961  | 482       | pir B36889 B368  | leuA protein, inactive - Lactococcus lactis subsp. lactis (strain IL1403)   | 75      | 63     |
| 793    | 1   | 1     | 1    | 180       | gi 143316  | [gap] gene products [Bacillus megaterium]                                   | 75      | 57     |
| 800    | 1   | 1     | 318  | 160       | gi 509411  | INFRA protein [Azorhizobium caulinodans]                                    | 75      | 34     |
| 811    | 1   | 1     | 1117 | 560       | gi 143434  | Rho Factor [Bacillus subtilis]  | 75      | 60     |
| 940    | 1   | 1     | 493  | 329       | gi 1276985   | Larginase [Bacillus caldovelox]   | 75      | 50     |
| 971    | 1   | 2     | 37   | 252       | gi 1001373   | Hypothetical protein [Synechocystis sp.]                                    | 75      | 58     |
| 1059   | 1   | 1     | 384  | 232       | gi 726480  | L-glutamine-D-fructose-6-phosphate amidotransferase [Bacillus subtilis]     | 75      | 67     |
| 1109   | 2   | 1     | 219  | 374       | gi 143331  | lalkaline phosphatase regulatory protein (Bacillus subtilis)                | 75      | 53     |
|        |     |       |      |           | pir A27650 A27650 regulatory protein phoR - Bacillus subtilis  |   |         | 156    |
|        |     |       |      |           | sp P23545 PHOR_BACSU ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN HOR (EC 2.7.3.-)  |   |         |        |
| 1268   | 1   | 1     | 271  | 137       | gi 300135  | ornithine acetyltransferase [Bacillus stearothermophilus]                   | 75      | 63     |
|        |     |       |      |           | sp Q07908 ARGJ_BACST GLUTAMATE N-ACETYLTRANSFERASE (EC 2.3.1.35) ORNITHINE ACETYLTRANSFERASE (ORNITHINE TRANSACETYLASE) (OATASE) / MINO-ACID |   |         | 135    |
|        |     |       |      |           | ACETYLTRANSFERASE (EC 2.3.1.1) (N-ACETYLGLUTAMATE YNTHA  |   |         |        |
| 1500   | 1   | 1     | 324  | 163       | gi 1225488   | lexinuclease ABC subunit B [Haemophilus influenzae]                         | 75      | 57     |
| 1529   | 1   | 1     | 798  | 400       | gi 1002521   | lMutL [Bacillus subtilis]   | 75      | 54     |
| 3010   | 1   | 1     | 770  | 387       | gi 1204435   | lpyruvate formate-lyase activating enzyme [Haemophilus influenzae]          | 75      | 54     |
| 3105   | 1   | 1     | 1    | 180       | gi 11041097  | lPyruvate Kinase [Bacillus psychrophilus]                                   | 75      | 57     |
| 3117   | 1   | 1     | 45   | 212       | gi 893317  | lpeptide synthetase module [Microcystis aeruginosa] pir S49111 S49111       | 75      | 42     |
|        |     |       |      |           | probable amino acid activating domain - icrocystis aeruginosa (fragment)   |   |         | 168    |
|        |     |       |      |           | (SUB 144-528)  |   |         |        |
| 3139   | 1   | 2     | 139  | 345       | gi 145294  | adenine phosphoribosyl-transferase [Escherichia coli]                       | 75      | 66     |
| 3880   | 1   | 1     | 618  | 310       | gi 1009366   | Respiratory nitrate reductase [Bacillus subtilis]                           | 75      | 58     |
| 3911   | 1   | 1     | 48   | 401       | gi 433991  | ATP synthase subunit beta [Bacillus subtilis]                               | 75      | 68     |
| 3957   | 1   | 1     | 2    | 379       | pir D36889 D368  | 3-isopropylmalate dehydratase (EC 4.2.1.33) chain leuC - Lactococcus lactis | 75      | 65     |
|        |     |       |      |           | subsp. lactis (strain IL1403)  |   |         | 378    |
| 4005   | 1   | 1     | 5    | 259       | gi 216746  | D-lactate dehydrogenase [Lactobacillus plantarum]                           | 75      | 48     |
| 4080   | 1   | 1     | 73   | 333       | gi 415855  | ldeoxyribose aldolase [Mycoplasma hominis]                                  | 75      | 59     |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop  | match      | match gene name   | % sim  | % ident | length |      |
|--------|-----|-------|-------|------------|---|--|---------|--------|------|
| ID     | ID  | (nt)  | (nt)  | accession  |   | (nt)   | (nt)    | (nt)   |      |
| 4111   | 1   | 1     | 339   | lgi 149435 | lputative [Lactococcus lactis]  | 75   | 57      | 339    |      |
| 4136   | 1   | 1     | 602   | 303        | lgi 450688  | lhsdM gene of Ecoprr1 gene product [Escherichia coli] pir S38437 S38437 hsdM | 75      | 56     |      |
|        |     |       |       |            |   |  |         | 300    |      |
|        |     |       |       |            | lputative [Escherichia coli pir S09629 S09629 hypothetical protein A - Escherichia coli (SUB 40-520)] |  |         |        |      |
| 4144   | 1   | 1     | 668   | 336        | lgi 48972   | lnitrate transporter [Synechococcus sp.]                                     | 75      | 49     | 333  |
| 4237   | 1   | 1     | 664   | 374        | lgi 1339950   | llarge subunit of NADH-dependent glutamate synthase [Plectonema boryanum]    | 75      | 55     | 291  |
| 4306   | 2   | 1     | 73    | 318        | lgi 294260  | lmajor surface glycoprotein [Pneumocystis carinii]                           | 75      | 68     | 246  |
| 4343   | 1   | 1     | 715   | 359        | lgi 1204652   | lmethylated-DNA--protein-cysteine methyltransferase [Haemophilus influenzae] | 75      | 52     | 357  |
| 4552   | 1   | 1     | 620   | 312        | lgi 296464  | lATPase [Lactococcus lactis]   | 75      | 55     | 309  |
| 38     | 9   | 1     | 5776  | 6126       | lgi 443793  | lNupC [Escherichia coli]   | 74      | 50     | 351  |
| 50     | 8   | 1     | 6910  | 6221       | lgi 1239988   | lhypothetical protein [Bacillus subtilis]                                    | 74      | 55     | 690  |
| 56     | 9   | 1     | 10770 | 12221      | lgi 1000451   | lTreP [Bacillus subtilis]  | 74      | 57     | 1452 |
| 64     | 2   | 1     | 2266  | 1622       | lgi 41015   | laspartate-tRNA ligase [Escherichia coli]                                    | 74      | 57     | 645  |
| 66     | 6   | 1     | 5063  | 4848       | lgi 1212729   | lYqhJ [Bacillus subtilis]  | 74      | 47     | 216  |
| 67     | 18  | 1     | 14334 | 14897      | lgi 1510631   | lendoglucanase [Methanococcus jannaschii]                                    | 74      | 52     | 564  |
| 102    | 15  | 1     | 12561 | 13136      | lgi 149429  | lputative [Lactococcus lactis]   | 74      | 67     | 576  |
| 102    | 16  | 1     | 13121 | 14419      | lgi 149435  | lputative [Lactococcus lactis]   | 74      | 57     | 1299 |
| 108    | 4   | 4873  | 3902  | lgi 39478  | lATP binding protein of transport ATPases [Bacillus firmus] ir S15486 S15486                          | 74   | 59      | 972    |      |
|        |     |       |       |            | lATP-binding protein - Bacillus firmus p P26946 YATR_BACFI HYPOTHETICAL                               |  |         |        |      |
|        |     |       |       |            | lATP-BINDING TRANSPORT PROTEIN.   |  |         |        |      |
| 116    | 5   | 1     | 8574  | 7093       | lgi 1205430   | ldipeptide transport system permease protein [Haemophilus influenzae]        | 74      | 49     | 1482 |
| 120    | 7   | 1     | 4342  | 4803       | lgi 146970  | lribonucleoside triphosphate reductase [Escherichia coli] pir A47331 A47331  | 74      | 58     | 462  |
|        |     |       |       |            | lanaerobic ribonucleotide reductase - Escherichia coli  |  |         |        |      |
| 121    | 7   | 1     | 5961  | 6581       | lgi 1107528   | lttg start [Campylobacter coli]  | 74      | 51     | 621  |
| 128    | 3   | 1     | 2320  | 3531       | lgi 143318  | lphosphoglycerate kinase [Bacillus megaterium]                               | 74      | 57     | 1212 |
| 130    | 7   | 1     | 5237  | 5791       | lgi 1256653   | lDNA-binding protein [Bacillus subtilis]                                     | 74      | 60     | 555  |
| 136    | 3   | 1     | 6745  | 5150       | lgi 143076  | lhistidase [Bacillus subtilis]   | 74      | 58     | 1596 |
| 145    | 2   | 1     | 664   | 1368       | lgi 407773  | ldevA gene product [Anabaena sp.]  | 74      | 45     | 705  |
| 152    | 1   | 1     | 552   | 277        | lgi 1377833   | lunknown [Bacillus subtilis]   | 74      | 54     | 276  |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop   | match       | match gene name   | % sim | % ident | length |
|--------|-----|--------|--------|-------------|---|-------|---------|--------|
| ID     | ID  | (nt)   | (nt)   | accession   |   | (nt)  |         | (nt)   |
| 164    | 10  | 111064 | 111375 | gi 580900   | ORF3 gene product [Bacillus subtilis]   | 1     | 74      | 52     |
| 175    | 2   | 3109   | 2624   | gi 642656   | lunknow [Rhizobium meliloti]  | 1     | 74      | 34     |
| 175    | 9   | 6064   | 5612   | gi 854656   | Na/H antiporter system ORF2 [Bacillus alcalophilus]   | 1     | 74      | 46     |
| 195    | 111 | 111346 | 10339  | gi 11204430 | hypothetical protein (SP: P23745) [Haemophilus influenzae]  | 1     | 74      | 55     |
| 205    | 117 | 9619   | 9059   | gi 1044979  | ribosomal protein L6 [Bacillus subtilis]  | 1     | 74      | 64     |
| 236    | 7   | 5574   | 6710   | gi 1146207  | putative [Bacillus subtilis]  | 1     | 74      | 63     |
| 241    | 3   | 4521   | 3334   | gi 694121   | malate thiokinase [Methylobacterium extorquens]   | 1     | 74      | 52     |
| 246    | 6   | 3305   | 2799   | gi 1467374  | single strand DNA binding protein [Bacillus subtilis]   | 1     | 74      | 64     |
| 249    | 4   | 6551   | 5313   | gi 1524397  | glycine betaine transporter OpU [Bacillus subtilis]   | 1     | 74      | 55     |
| 261    | 7   | 4389   | 4081   | gi 809542   | CbrB protein [Erwinia chrysanthemi]   | 1     | 74      | 42     |
| 278    | 6   | 5714   | 4665   | gi 1204872  | ATP-binding protein [Haemophilus influenzae]  | 1     | 74      | 54     |
| 309    | 1   | 1220   | 666    | gi 1205579  | hypothetical protein (GB:U14003_302) [Haemophilus influenzae]   | 1     | 74      | 53     |
| 315    | 2   | 1473   | 862    | gi 143398   | quinol oxidase [Bacillus subtilis]  | 1     | 74      | 57     |
| 320    | 1   | 1      | 1065   | gi 143389   | glutaminase of carbamyl phosphate synthetase [Bacillus subtilis]  | 1     | 74      | 60     |
| 380    | 2   | 382    | 1128   | gi 534857   | pir E39845 E39845 carbamoyl-phosphate synthase glutamine-hydrolyzing (EC 6.3.5.5), pyrimidine-repressible, small hain - Bacillus subtilis | 1     | 74      | 56     |
| 405    | 2   | 1742   | 1311   | gi 1303915  | ATPase subunit a [Bacillus stearothermophilus]  | 1     | 74      | 65     |
| 433    | 5   | 2503   | 3270   | gi 4733902  | Yqhz [Bacillus subtilis]  | 1     | 74      | 56     |
| 452    | 1   | 1      | 942    | gi 413982   | alpha-acetolactate synthase [Lactococcus lactis]  | 1     | 74      | 52     |
| 461    | 1   | 1      | 3      | gi 558494   | lipa-58r gene product [Bacillus subtilis]   | 1     | 74      | 942    |
| 462    | 2   | 1174   | 1407   | gi 40211    | thiostreine synthase (thrc) (AA 1-352) [Bacillus subtilis] ir A25364 A25364   | 1     | 74      | 56     |
| 478    | 1   | 574    | 320    | gi 1499005  | threonine synthase (EC 4.2.99.2) - Bacillus subtilis  | 1     | 74      | 52     |
| 501    | 2   | 739    | 1740   | gi 217040   | thioredoxin [Bacillus subtilis]   | 1     | 74      | 62     |
| 551    | 2   | 4083   | 2791   | gi 143040   | thiostreine synthase [Methanococcus jannaschii]   | 1     | 74      | 234    |
|        |     |        |        |             | glucosidase [Streptococcus pyogenes]  | 1     | 74      | 58     |
|        |     |        |        |             | lacid glycoprotein [Bacillus subtilis]  | 1     | 74      | 1002   |
|        |     |        |        |             | glutamate-1-semialdehyde 2,1-aminotransferase [Bacillus subtilis]   | 1     | 74      | 51     |
|        |     |        |        |             | pir D42728 D42728 glutamate-1-semialdehyde 2,1-aminotransferase (EC 4.3.8) -  | 1     | 74      | 1293   |
|        |     |        |        |             | Bacillus subtilis   | 1     | 74      | -      |

*S. aureus* - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | ID   | Start | Stop | match accession | match gene name  | % sim | % ident | length | (nt) |
|--------|-----|------|-------|------|-----------------|--|-------|---------|--------|------|
|        |     |      | (nt)  | (nt) |                 |  |       |         |        |      |
| 573    | 1   | 1    | 1     | 477  | gi 1006605      | hypothetical protein [Synechocystis sp.]   | 74    | 45      | 477    |      |
| 596    | 2   | 1780 | 1298  | 1298 | gi 1303853      | Yqgf [Bacillus subtilis]   | 74    | 55      | 483    |      |
| 618    | 2   | 2924 | 1758  | 1758 | gi 1146237      | 21.4% of identity to trans-acting transcription factor of <i>Sacharomyces cerevisiae</i> ; 25% of identity to sucrose synthase of <i>Zea mays</i> ; putative [Bacillus subtilis] | 74    | 55      | 1167   |      |
| 659    | 2   | 1269 | 1595  | 1595 | gi 1072380      | ORF3 [Lactococcus lactis]  | 74    | 62      | 327    |      |
| 724    | 1   | 373  | 188   | 188  | gi 143374       | phosphoribosyl glycaminide synthetase (PUR-D; gtg start codon) Bacillus subtilis]  | 74    | 58      | 186    |      |
| 743    | 2   | 604  | 1209  | 1209 | gi 153833       | ORF1; putative [Streptococcus parasanguis]   | 74    | 50      | 606    |      |
| 836    | 1   | 1    | 2     | 259  | gi 143458       | ORF V [Bacillus subtilis]  | 74    | 47      | 258    |      |
| 989    | 2   | 443  | 724   | 724  | gi 1303994      | YqkM [Bacillus subtilis]   | 74    | 46      | 282    |      |
| 1106   | 1   | 1    | 1     | 492  | gi 46970        | lepid gene product [Staphylococcus epidermidis]  | 74    | 54      | 492    |      |
| 1135   | 2   | 373  | 528   | 528  | gi 1413948      | lipa-24d gene product [Bacillus subtilis]  | 74    | 48      | 156    |      |
| 1234   | 1   | 817  | 452   | 452  | gi 495245       | lrecJ gene product [Erwinia chrysanthemi]  | 74    | 36      | 366    |      |
| 2586   | 1   | 2    | 238   | 238  | gi 1149701      | lsbcc gene product [Clostridium perfringens]   | 74    | 62      | 237    |      |
| 2959   | 1   | 798  | 400   | 400  | gi 1405454      | laconitase [Bacillus subtilis]   | 74    | 60      | 399    |      |
| 2962   | 1   | 650  | 363   | 363  | gi 450686       | 13-phosphoglycerate kinase [Thermotoga maritima]   | 74    | 58      | 288    |      |
| 2983   | 1   | 3    | 191   | 191  | gi 1303893      | YqhL [Bacillus subtilis]   | 74    | 56      | 189    |      |
| 3018   | 1   | 2    | 223   | 223  | gi 143040       | glutamate-1-semialdehyde 2,1-aminotransferase [Bacillus subtilis]  | 74    | 56      | 222    |      |
| 4035   | 1   | 184  | 360   | 360  | gi 1022725      | lunkown [Staphylococcus haemolyticus]  | 74    | 64      | 177    |      |
| 4045   | 1   | 607  | 305   | 305  | gi 1510977      | [M. jannaschii predicted coding region MJ0938 [Methanococcus jannaschii]   | 74    | 41      | 303    |      |
| 4283   | 1   | 471  | 304   | 304  | gi 520844       | orf4 [Bacillus subtilis]   | 74    | 58      | 168    |      |
| 4449   | 1   | 3    | 221   | 221  | gi 580910       | peptide-synthetase ORF1 [Bacillus subtilis]  | 74    | 54      | 219    |      |
| 4587   | 1   | 458  | 231   | 231  | gi 1370207      | orf6 [Lactobacillus sake]  | 74    | 59      | 228    |      |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop   | match<br>accession | match gene name   | % sim | % ident | length<br>(nt) |
|--------|-----|--------|--------|--------------------|---|-------|---------|----------------|
| ID     | ID  | (nt)   | (nt)   |                    |   |       |         |                |
| 4603   | 1   | 29     | 214    | gi 146208          | glutamate synthase large subunit (EC 2.6.1.53) [Escherichia coli] pir A29617 A29617 glutamate synthase (NADPH) (EC 1.4.1.13) large chain - Escherichia coli | 74    | 60      | 186            |
| 4670   | 1   | 366    | 184    | gi 1256135         | YbbF [Bacillus subtilis]  | 74    | 61      | 183            |
| 5      | 10  | 7953   | 7162   | gi 143727          | putative [Bacillus subtilis]  | 73    | 42      | 792            |
| 11     | 2   | 2454   | 1372   | gi 166338          | dihydroorotate dehydrogenase [Agrocybe aegerita]  | 73    | 55      | 1083           |
| 14     | 1   | 2024   | 1020   | gi 1433373         | phosphoribosyl aminoimidazole carboxy formyl ormyltransferase/inosine monophosphate cyclohydrolase (PUR-H(J)) Bacillus subtilis                             | 73    | 54      | 1005           |
| 23     | 5   | 5426   | 4635   | gi 1468939         | meso-2,3-butanediol dehydrogenase (D-acetoin forming) [Klebsiella pneumoniae]   | 73    | 58      | 792            |
| 23     | 17  | 117379 | 16360  | gi 1297060         | ornithine cyclodeaminase [Rhizobium meliloti]   | 73    | 37      | 1020           |
| 29     | 2   | 692    | 1273   | gi 467442          | stage V sporulation [Bacillus subtilis]   | 73    | 54      | 582            |
| 31     | 5   | 6467   | 4914   | gi 1414000         | lipa-76d gene product [Bacillus subtilis]   | 73    | 55      | 1554           |
| 37     | 8   | 8658   | 7402   | gi 1429259         | ipePT gene product [Bacillus subtilis]  | 73    | 59      | 1257           |
| 37     | 9   | 7738   | 7562   | gi 168367          | alpha-isopropylmalate isomerase (put.); putative [Rhizomucor ircinelloides]   | 73    | 52      | 177            |
| 38     | 7   | 3931   | 4896   | gi 405885          | lyeIN [Escherichia coli]  | 73    | 58      | 966            |
| 44     | 6   | 5041   | 4238   | gi 580895          | unknown [Bacillus subtilis]   | 73    | 53      | 804            |
| 44     | 11  | 7767   | 8306   | gi 42009           | lmoAB gene product [Escherichia coli]   | 73    | 50      | 540            |
| 45     | 3   | 2439   | 3080   | gi 1109685         | Prow [Bacillus subtilis]  | 73    | 47      | 642            |
| 54     | 13  | 114036 | 113794 | gi 413931          | lipa-7d gene product [Bacillus subtilis]  | 73    | 61      | 243            |
| 59     | 4   | 1430   | 2248   | gi 147923          | threonine dehydratase 2 (EC 4.2.1.16) [Escherichia coli]  | 73    | 53      | 819            |
| 65     | 1   | 1458   | 730    | gi 677944          | AppF [Bacillus subtilis]  | 73    | 56      | 729            |
| 80     | 2   | 1375   | 860    | gi 580932          | lmurD gene product [Bacillus subtilis]  | 73    | 53      | 516            |
| 102    | 13  | 10124  | 11179  | gi 580891          | 3-isopropylmalate dehydrogenase (AA 1 - 365) (Bacillus subtilis) pir A26522 A26522 3-isopropylmalate dehydrogenase (EC 1.1.1.85) - acillus subtilis         | 73    | 55      | 1056           |
| 109    | 2   | 3493   | 2600   | gi 1510849         | M. jannaschii predicted coding region MJ0775 (Methanococcus jannaschii)   | 73    | 40      | 894            |
| 120    | 8   | 4782   | 5756   | gi 146970          | ribonucleoside triphosphate reductase [Escherichia coli] pir A47331 A47331 anaerobic ribonucleotide reductase - Escherichia coli                            | 73    | 56      | 975            |
| 120    | 9   | 5726   | 6223   | gi 1204333         | lanaerobic ribonucleoside-triphosphate reductase [Haemophilus influenzae]   | 73    | 62      | 498            |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop | match     | gene name  | % sim   | % ident | length |      |
|--------|-----|-------|------|-----------|--|---|---------|--------|------|
| ID     | ID  | (nt)  | (nt) | accession |  |   |         | (nt)   |      |
| 1      | 132 | 5     | 4151 | 4363      | gi 871048  | HPSR2 - heavy chain potential motor protein [Giardia intestinalis]      | 73      | 43     | 213  |
| 1      | 140 | 6     | 5952 | 4324      | gi 634107  | kdpB [Escherichia coli]   | 73      | 59     | 1629 |
| 1      | 142 | 6     | 7060 | 5939      | gi 410125  | ribG gene product [Bacillus subtilis]                                   | 73      | 57     | 1122 |
| 1      | 149 | 4     | 1866 | 1717      | gi 460892  | heparin binding protein-44, HBP-44 [mice, Peptide, 360 aa]              | 73      | 53     | 150  |
|        |     |       |      |           | pir JX0281 JX0281 heparin-binding protein-44 precursor - mouse | gi 220434   |         |        |      |
|        |     |       |      |           | ORF [Mus musculus] (SUB 2-360)                                 |   |         |        |      |
| 1      | 158 | 1     | 1    | 1431      | gi 882504  | ORF f560 [Escherichia coli]   | 73      | 57     | 1431 |
| 1      | 174 | 6     | 5352 | 4525      | gi 1146240   | ketopantoate hydroxymethyltransferase [Bacillus subtilis]               | 73      | 55     | 828  |
| 1      | 175 | 8     | 5537 | 5178      | gi 854657  | Na/H antiporter system ORF3 [Bacillus alcalophilus]                     | 73      | 56     | 360  |
| 1      | 186 | 5     | 6593 | 5493      | gi 467477  | unknown [Bacillus subtilis]   | 73      | 48     | 1101 |
| 1      | 249 | 6     | 6283 | 5729      | gi 1524397   | glycine betaine transporter Opd [Bacillus subtilis]                     | 73      | 56     | 555  |
| 1      | 265 | 4     | 1873 | 2280      | gi 39848   | U3 [Bacillus subtilis]  | 73      | 41     | 408  |
| 1      | 270 | 1     | 328  | 582       | gi 780461  | 1220 kDa polyprotein [African swine fever virus]                        | 73      | 53     | 255  |
| 1      | 278 | 4     | 4283 | 3618      | gi 1208965   | hypothetical 23.3 kd protein [Escherichia coli]                         | 73      | 49     | 666  |
| 1      | 279 | 3     | 4984 | 3593      | gi 1185288   | isochorismate synthase [Bacillus subtilis]                              | 73      | 58     | 1392 |
| 1      | 291 | 4     | 1207 | 1575      | gi 1511440   | glutamine--fructose-6-phosphate transaminase [Methanococcus jannaschii] | 73      | 63     | 369  |
| 1      | 299 | 2     | 735  | 1166      | gi 467437  | unknown [Bacillus subtilis]   | 73      | 58     | 432  |
| 1      | 299 | 5     | 2050 | 3234      | gi 467439  | temperature sensitive cell division [Bacillus subtilis]                 | 73      | 53     | 1185 |
| 1      | 334 | 1     | 1237 | 728       | gi 536655  | ORF YBR244W [Saccharomyces cerevisiae]                                  | 73      | 43     | 510  |
| 1      | 336 | 2     | 1827 | 1036      | gi 790943  | urea amidolyase [Bacillus subtilis]                                     | 73      | 51     | 792  |
| 1      | 374 | 3     | 1389 | 1874      | gi 1405451   | YneJ [Bacillus subtilis]  | 73      | 55     | 486  |
| 1      | 433 | 4     | 1916 | 2554      | gi 473902  | alpha-acetolactate synthase [Lactococcus lactis]                        | 73      | 54     | 639  |
| 1      | 509 | 2     | 1795 | 1028      | gi 467483  | unknown [Bacillus subtilis]   | 73      | 56     | 768  |
| 1      | 513 | 1     | 1709 | 918       | gi 1146220   | NAD+ dependent glycerol-3-phosphate dehydrogenase [Bacillus subtilis]   | 73      | 56     | 792  |
| 1      | 533 | 2     | 239  | 733       | gi 1510605   | hypothetical protein (SP:P42297) [Methanococcus jannaschii]             | 73      | 44     | 495  |
| 1      | 546 | 2     | 1148 | 2815      | gi 41748   | hsdM protein (AA 1-520) [Escherichia coli]                              | 73      | 52     | 1668 |
| 1      | 549 | 1     | 762  | 382       | gi 1314847   | CinA [Bacillus subtilis]  | 73      | 57     | 381  |
| 1      | 567 | 1     | 1346 | 675       | gi 410137  | ORFX13 [Bacillus subtilis]  | 73      | 58     | 672  |

## S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop | match      | match gene name   | % sim | % ident | length |
|--------|-----|-------|------|------------|---|-------|---------|--------|
| ID     | ID  | (nt)  | (nt) | accession  |   | (nt)  | (nt)    |        |
| 716    | 2   | 654   | 1112 | gi 1256623 | exo-deoxyribonuclease [Bacillus subtilis]   | 73    | 56      | 459    |
| 772    | 1   | 3     | 677  | gi 142010  | Shows 70.2% similarity and 48.6% identity to the EnvM protein of almonella  | 73    | 57      | 675    |
| 774    | 1   | 3     | 209  | gi 409286  | lbumU [Bacillus subtilis]   | 73    | 52      | 207    |
| 782    | 1   | 1     | 402  | gi 143320  | [gap] gene products [Bacillus megaterium]   | 73    | 56      | 402    |
| 789    | 2   | 451   | 762  | gi 1063246 | low homology to P14 protein of <i>Neamophilus influenzae</i> and 14.2 kDa protein of <i>Escherichia coli</i> [Bacillus subtilis]        | 73    | 56      | 312    |
| 796    | 1   | 3     | 911  | gi 853754  | ABC transporter [Bacillus subtilis]   | 73    | 58      | 909    |
| 806    | 3   | 1209  | 949  | gi 143786  | tryptophanyl-tRNA synthetase (EC 6.1.1.2) [Bacillus subtilis] pir JT0481 YWBS tryptophanyl-tRNA ligase (EC 6.1.1.2) - Bacillus subtilis | 73    | 51      | 261    |
| 816    | 2   | 4839  | 3097 | gi 41748   | hsdM protein (AA 1-520) [Escherichia coli]  | 73    | 52      | 1743   |
| 839    | 1   | 798   | 400  | gi 886906  | argininosuccinate synthetase [Streptomyces clavuligerus] pir S5759 S57659   | 73    | 59      | 399    |
| 857    | 1   | 3     | 290  | gi 348052  | acetoin utilization protein [Bacillus subtilis]   | 73    | 50      | 288    |
| 1008   | 1   | 790   | 398  | gi 40100   | lrodC (tag3) polypeptide (AA 1-746) [Bacillus subtilis] ir S06049 S06049  | 73    | 41      | 393    |
| 1018   | 1   | 1     | 213  | gi 529357  | [No definition line found [Caenorhabditis elegans] sp P46975 STT3_CAEEL   | 73    | 53      | 213    |
| 1033   | 1   | 3     | 491  | gi 142706  | OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT OMOLOG.   | 73    | 51      | 489    |
| 1174   | 1   | 395   | 204  | gi 1149513 | lcomG1 gene product [Bacillus subtilis]   | 73    | 60      | 192    |
| 1175   | 1   | 655   | 329  | gi 473817  | alpha3a subunit of laminin 5 [Homo sapiens]   | 73    | 57      | 327    |
| 1187   | 1   | 3     | 209  | gi 580870  | 'ORF' [Escherichia coli]  | 73    | 52      | 207    |
| 1206   | 1   | 72    | 245  | gi 144816  | lipa-37d qoxA gene product [Bacillus subtilis]  | 73    | 43      | 174    |
| 1454   | 1   | 423   | 241  | gi 1213253 | [Moorella thermoacetica]  | 73    | 53      | 183    |
| 1469   | 1   | 517   | 260  | gi 1303787 | Unknown [Schizosaccharomyces pombe]   | 73    | 55      | 258    |
| 1761   | 1   | 374   | 189  | gi 9135    | [YqeG [Bacillus subtilis]]  | 73    | 34      | 186    |
| 1849   | 1   | 467   | 243  | gi 1162307 | Mst26Aa gene product [Drosophila simulans]  | 73    | 60      | 225    |
| 2055   | 1   | 2     | 400  | gi 559381  | DNase II [Trypanosoma cruzi]  | 73    | 34      | 399    |
| 2556   | 1   | 2     | 244  | gi 145925  | P47K protein [Rhodococcus erythropolis]   | 73    | 62      | 243    |
|        |     |       |      |            | [fecB [Escherichia coli]]   |       |         |        |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop  | match            | match gene name  | % sim | % ident | length |
|--------|-----|-------|-------|------------------|--|-------|---------|--------|
| ID     | ID  | (nt)  | (nt)  | accession        |  | (nt)  | (nt)    | (nt)   |
| 2947   | 2   | 549   | 400   | lgi 1184680      | polynucleotide phosphorylase [Bacillus subtilis]   | 73    | 51      | 150    |
| 2956   | 1   | 746   | 375   | lgi 143397       | quinol oxidase [Bacillus subtilis]   | 73    | 58      | 372    |
| 3037   | 1   | 655   | 329   | lgi 143091       | lactolactate synthase [Bacillus subtilis]  | 73    | 55      | 327    |
| 3115   | 1   | 385   | 194   | lgi 323866       | overlapping out-of-phase protein [Eggplant mosaic virus]<br>sp P20129 V70K_EPMV_70_KD PROTEIN.   | 73    | 53      | 192    |
| 3603   | 2   | 700   | 527   | lgi 1439521      | lglutaryl-CoA dehydrogenase precursor [Mus musculus]   | 73    | 48      | 174    |
| 3743   | 1   | 798   | 400   | lgi 450688       | lhsdM gene of EcoprrI gene product [Escherichia coli] pir S38437 S38437_hsdM<br>protein - Escherichia coli pir S09629 S09629 hypothetical protein A -<br>Escherichia coli (SUB 40-520) | 73    | 54      | 399    |
| 3752   | 1   | 640   | 359   | lgi 1524193      | unknown [Mycobacterium tuberculosis]   | 73    | 59      | 282    |
| 3852   | 1   | 2     | 181   | lgi 216746       | D-lactate dehydrogenase [Lactobacillus plantarum]  | 73    | 68      | 180    |
| 3914   | 1   | 475   | 239   | lpir S13490 S134 | Hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) - Chicken (fragment)   | 73    | 53      | 237    |
| 3914   | 2   | 570   | 343   | lgi 528991       | unknown [Bacillus subtilis]  | 73    | 38      | 228    |
| 4069   | 1   | 2     | 316   | lgi 40003        | oxoglutarate dehydrogenase (NADP+) [Bacillus subtilis] P P23129 ODO1_BACSU<br>2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (EC 2.4.2) (ALPHA- KETOGLUTARATE<br>DEHYDROGENASE).            | 73    | 55      | 315    |
| 4165   | 1   | 715   | 365   | lgi 1439521      | lglutaryl-CoA dehydrogenase precursor [Mus musculus]   | 73    | 48      | 351    |
| 4196   | 1   | 1     | 177   | lgi 809660       | deoxyribose-phosphate aldolase [Bacillus subtilis] Pir S49455 S49455<br>deoxyribose-phosphate aldolase (EC 4.1.2.4) - acillus subtilis   | 73    | 60      | 177    |
| 4202   | 1   | 572   | 378   | lgi 528991       | unknown [Bacillus subtilis]  | 73    | 38      | 195    |
| 4314   | 1   | 2     | 193   | lgi 436797       | N-acyl-L-amino acid amidohydrolase [Bacillus stearothermophilus]<br>sp P37112 AMA_BACST_N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 5.1.14)<br>(AMINOACYLASE).                              | 73    | 47      | 192    |
| 4393   | 1   | 3     | 263   | lgi 216267       | lORF2 [Bacillus megaterium]  | 73    | 47      | 261    |
| 35     | 2   | 903   | 1973  | lgi 1146196      | phosphoglycerate dehydrogenase [Bacillus subtilis]   | 72    | 53      | 1071   |
| 38     | 22  | 19094 | 17877 | lgi 602031       | similar to trimethylamine DH [Mycoplasma capricolum] pir S49950 S49950<br>probable trimethylamine dehydrogenase (EC 5.99.7) - Mycoplasma capricolum<br>(SGC3) (fragment)               | 72    | 54      | 1218   |
| 38     | 123 | 18134 | 19162 | lgi 413968       | lipa-44d gene product [Bacillus subtilis]  | 72    | 54      | 1029   |
| 44     | 119 | 11895 | 12953 | lgi 516272       | unknown [Bacillus subtilis]  | 72    | 49      | 1059   |
| 48     | 7   | 6248  | 7117  | lgi 43499        | pyruvate synthase [Halobacterium halobium]   | 72    | 49      | 870    |
| 50     | 7   | 6563  | 5691  | lgi 11205399     | proton glutamate symport protein [Haemophilus influenzae]  | 72    | 53      | 873    |

## S. aureus - Putative coding regions of novel proteins similar to known proteins

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|--------|-----|--------|--------|------------|-----------------------------|--|--|---------|--------|----|
|        |     | ID     | (nt)   | (nt)       | accession                   |  |  |         | (nt)   |    |
| 53     | 9   | 110521 | 1      | 9259       | gi 1303956                  | YqjE [Bacillus subtilis]   | 1  | 72      | 52     |    |
| 56     | 123 | 129549 | 129995 | 1gi 467471 | unknown [Bacillus subtilis] |  | 1  | 72      | 47     |    |
| 69     | 4   | 5298   | 1      | 4123       | gi 1354775                  | lpf05/R [Treponema pallidum]   | 1  | 72      | 46     |    |
| 69     | 5   | 4377   | 1      | 4982       | gi 904198                   | hypothetical protein [Bacillus subtilis]   | 1  | 72      | 43     |    |
| 73     | 1   | 1      | 2      | 1          | 856                         | gi 142997  | 1glycerol uptake facilitator [Bacillus subtilis]                             | 1       | 72     | 59 |
| 98     | 113 | 9371   | 1      | 10258      | gi 467435                   | unknown [Bacillus subtilis]  | 1  | 72      | 50     |    |
| 127    | 1   | 1      | 1      | 1          | 1593                        | gi 217144  | 1alanine carrier protein [thermophilic bacterium PS3] pir A45111 A45111      | 1       | 72     | 56 |
|        |     |        |        |            |                             |  | 1alanine transport protein - thermophilic acterium PS-3                      |         |        |    |
| 131    | 1   | 5197   | 1      | 2600       | gi 153952                   | 1polymerase III polymerase subunit (dnaE) [Salmonella typhimurium] pir A45915 A45915 DNA-directed DNA polymerase (EC 2.7.7.7) III lpha chain | 1  | 72      | 53     |    |
|        |     |        |        |            |                             |  | - Salmonella typhimurium   |         |        |    |
| 141    | 4   | 1040   | 1      | 1978       | gi 1405446                  | 1transketolase [Bacillus subtilis]   | 1  | 72      | 54     |    |
| 149    | 8   | 2819   | 1      | 2535       | gi 1606234                  | 1secY [Escherichia coli]   | 1  | 72      | 44     |    |
| 149    | 117 | 5472   | 1      | 5245       | gi 1304472                  | 1DNA polymerase [Unidentified phycodnavirus clone OTU4]  | 1  | 72      | 55     |    |
| 154    | 1   | 1      | 1      | 210        | gi 1205620                  | 1ferritin like protein [Haemophilus influenzae]  | 1  | 72      | 40     |    |
| 155    | 1   | 2207   | 1      | 1320       | gi 3991610                  | 1farnesyl diphosphate synthase [Bacillus stearothermophilus] pir JX0257 JX0257 geranyl-transtransferase (EC 2.5.1.10) - Bacillus             | 1  | 72      | 57     |    |
|        |     |        |        |            |                             |  | - teatothermophilus  |         |        |    |
| 180    | 1   | 1      | 2      | 1          | 328                         | gi 433630  | 1A180 [Saccharomyces cerevisiae]   | 1       | 72     | 62 |
| 184    | 3   | 1145   | 1      | 3553       | gi 1205110                  | 1virulence associated protein homolog [Haemophilus influenzae]   | 1  | 72      | 49     |    |
| 195    | 2   | 1923   | 1      | 1279       | gi 1001730                  | 1hypothetical protein [Synchocystis sp.]   | 1  | 72      | 45     |    |
| 206    | 113 | 114646 | 1      | 15869      | gi 1064807                  | 1ORTHININE AMINOTRANSFERASE [Bacillus subtilis]  | 1  | 72      | 50     |    |
| 209    | 2   | 462    | 1      | 932        | gi 1204666                  | 1hypothetical protein (GB:XY3124_53) [Haemophilus influenzae]  | 1  | 72      | 60     |    |
| 215    | 2   | 764    | 1      | 522        | gi 881513                   | 1insulin receptor homolog [Drosophila melanogaster] pir S57245 S57245  | 1  | 72      | 63     |    |
|        |     |        |        |            |                             | 1insulin receptor homolog - fruit fly (Drosophila melanogaster) (SUB 46-2146)  |  |         |        |    |
| 224    | 1   | 1      | 2      | 1          | 790                         | gi 949974  | 1sucrose repressor [Staphylococcus xylosus]                                  | 1       | 72     | 54 |
| 233    | 1   | 1      | 1526   | 1          | 765                         | gi 1408493   | 1homologous to SwissProt:YIDA_ECOLI hypothetical protein [Bacillus subtilis] | 1       | 72     | 52 |
| 240    | 1   | 1      | 220    | 1          | 1485                        | gi 537049  | 1ORF_0470 [Escherichia coli]   | 1       | 72     | 52 |
| 245    | 1   | 1      | 3      | 1          | 1340                        | gi 1204578   | 1hypothetical protein (GB:U06949_1) [Haemophilus influenzae]                 | 1       | 72     | 46 |

S. aureus - Putative coding regions of novel proteins similar to known proteins

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|--------|-----|-------|--------|-----------|------------------|---|---------|--------|
| ID     | ID  | (nt)  | (nt)   | accession |                  | (nt)  | (nt)    | (nt)   |
| 259    | 1   | 2     | 2108   | 1245      | lgi 1340128      | ORF1 [Staphylococcus aureus]  | 72      | 59     |
| 304    | 1   | 2     | 285    | 1094      | lgi 1205330      | lglutamine-binding periplasmic protein [Haemophilus influenzae]   | 72      | 52     |
| 307    | 1   | 10    | 5326   | 5039      | lgi 1070015      | lprotein-dependent [Bacillus subtilis]  | 72      | 53     |
| 315    | 1   | 1     | 517    | 260       | lgi 1433999      | lquinol oxidase [Bacillus subtilis]   | 72      | 55     |
| 316    | 1   | 11    | 9622   | 9308      | lgi 1204445      | lhypothetical protein (SP:P27857) [Haemophilus influenzae]  | 72      | 52     |
| 337    | 1   | 3     | 926    | 1609      | lgi 487433       | lcitrate synthase II [Bacillus subtilis]  | 72      | 55     |
| 364    | 1   | 7     | 112538 | 110493    | lgi 1510643      | lferrous iron transport protein B [Methanococcus jannaschii]  | 72      | 53     |
| 409    | 1   | 2     | 340    | 1263      | lgi 1402944      | lorfM1 gene product [Bacillus subtilis]   | 72      | 49     |
| 441    | 1   | 3     | 2177   | 1590      | lgi 312379       | lhighly conserved among eubacteria [Clostridium acetobutylicum]   | 72      | 48     |
| 453    | 1   | 6     | 2654   | 2505      | lpir S00601 BXSA | lantibacterial protein 3 - Staphylococcus haemolyticus  | 72      | 588    |
| 460    | 1   | 1     | 2      | 625       | lgi 1016162      | lABC transporter subunit [Cyanophora paradoxa]  | 72      | 51     |
| 463    | 1   | 1     | 3253   | 1628      | lgi 666014       | lThe polymorphism (RFLP) of this gene is associated with susceptibility to essential hypertension. The SA gene product has light homology to acetyl-CoA synthetase [Homo sapiens] | 72      | 60     |
| 480    | 1   | 4     | 3047   | 3466      | lgi 433992       | lATP synthase subunit epsilon [Bacillus subtilis]   | 72      | 53     |
| 502    | 1   | 1     | 1086   | 586       | lgi 310859       | lORF2 [Synechococcus sp.]   | 72      | 50     |
| 519    | 1   | 1     | 81     | 1184      | lgi 1303704      | lYrkE [Bacillus subtilis]   | 72      | 54     |
| 559    | 1   | 1     | 3      | 746       | lgi 1107530      | lceUD gene product [Campylobacter coli]   | 72      | 56     |
| 575    | 1   | 1     | 1142   | 573       | lgi 1303866      | lYqgs [Bacillus subtilis]   | 72      | 56     |
| 671    | 1   | 1     | 2      | 592       | lgi 1204497      | lprotein-export membrane protein [Haemophilus influenzae]   | 72      | 44     |
| 679    | 1   | 2     | 295    | 1251      | lgi 563258       | lvirulence-associated protein E [Dichelobacter nodosus]   | 72      | 52     |
| 687    | 1   | 2     | 295    | 957       | lgi 1146214      | l44% identical amino acids with the Escherichia coli smba suppressive putative [Bacillus subtilis]  | 72      | 49     |
| 837    | 1   | 1     | 1      | 435       | lgi 1146183      | lputative [Bacillus subtilis]   | 72      | 54     |
| 868    | 1   | 1     | 150    | 788       | lgi 1377842      | lunknown [Bacillus subtilis]  | 72      | 55     |
| 922    | 1   | 1     | 130    | 432       | lgi 1088269      | lunknown protein [Azotobacter vinelandii]   | 72      | 58     |
| 941    | 1   | 1     | 2      | 238       | lgi 153929       | lNADPH-sulfite reductase flavoprotein component [Salmonella typhimurium]  | 72      | 49     |
| 980    | 1   | 1     | 840    | 421       | lgi 853767       | lUDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus subtilis]  | 72      | 59     |

S. aureus - Putative coding regions of novel proteins similar to known proteins

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|--------|-----|--------|--------|-----------------|---|-------|---------|--------|
| ID     | ID  | (nt)   | (nt)   | accession       |   | (nt)  | (nt)    | (nt)   |
| 1209   | 1   | 383    | 213    | lgi 144735      | neurotoxin type B [Clostridium botulinum]   | 72    | 44      | 171    |
| 1469   | 2   | 671    | 474    | lgi 1205458     | hypothetical protein (GB:D26562_47) [Haemophilus influenzae]  | 72    | 63      | 198    |
| 1956   | 1   | 727    | 365    | lgi 154409      | hexosephosphate transport protein [Salmonella typhimurium]  | 72    | 44      | 363    |
|        |     |        |        |                 | pir B41853 B41853 hexose phosphate transport system regulatory rotein uhPB                          |       |         |        |
|        |     |        |        |                 | - Salmonella typhimurium  |       |         |        |
| 2101   | 1   | 3      | 401    | lgi 1303950     | Yqiy [Bacillus subtilis]  | 72    | 50      | 399    |
| 2503   | 1   | 569    | 399    | lgi 149713      | formate dehydrogenase [Methanobacterium formicum] pir A42712 A42712                                 | 72    | 56      | 171    |
|        |     |        |        |                 | - formate dehydrogenase (EC 1.2.1.2) - ethanobacterium formicum                                     |       |         |        |
| 2967   | 1   | 3      | 155    | lgi 1212729     | YqhJ [Bacillus subtilis]  | 72    | 46      | 153    |
| 3004   | 1   | 367    | 185    | lgi 665999      | hypothetical protein [Bacillus subtilis]  | 72    | 55      | 183    |
| 3109   | 1   | 278    | 141    | lgi 413968      | lipa-44d gene product [Bacillus subtilis]   | 72    | 45      | 138    |
| 3171   | 1   | 3      | 287    | lgi 515938      | glutamate synthase (ferredoxin) [Synechocystis sp.] pir S46957 S16957                               | 72    | 52      | 285    |
|        |     |        |        |                 | - glutamate synthase (ferredoxin) (EC 1.4.7.1) - ynechocystis sp.                                   |       |         |        |
| 3771   | 1   | 26     | 367    | lgi 1408501     | homologous to N-acyl-L-amino acid amidohydrolase of Bacillus stearothermophilus [Bacillus subtilis] | 72    | 63      | 342    |
| 3951   | 1   | 1      | 222    | lgi 1500409     | M. jannaschii predicted coding region MJ1519 [Methanococcus jannaschii]                             | 72    | 38      | 222    |
| 4190   | 1   | 721    | 362    | lgi 39956       | lIGlc [Bacillus subtilis]   | 72    | 57      | 360    |
| 4444   | 1   | 3      | 347    | lgi 1009366     | Respiratory nitrate reductase [Bacillus subtilis]   | 72    | 55      | 345    |
| 6      | 2   | 931    | 1200   | lgi 537095      | ornithine carbamoyltransferase [Escherichia coli]   | 71    | 55      | 270    |
| 11     | 15  | 111350 | 10859  | lgi 532309      | 125 kDa protein [Escherichia coli]  | 71    | 47      | 492    |
| 19     | 2   | 1248   | 2435   | lgi 1244574     | D-alanine:D-alanine ligase [Enterococcus hirae]   | 71    | 52      | 1188   |
| 21     | 2   | 898    | 1488   | lgi 149629      | anthranilate synthase component 2 [Leptospira biflexa] pir C32840 C32840                            | 71    | 45      | 591    |
|        |     |        |        |                 | - anthranilate synthase (EC 4.1.3.27) component II Leptospira biflexa                               |       |         |        |
| 34     | 1   | 1      | 567    | lgi 1303983     | YqkF [Bacillus subtilis]  | 71    | 59      | 567    |
| 37     | 3   | 3192   | 2806   | lgi 1209681     | glutamate-rich protein [Bacillus firmus]  | 71    | 50      | 387    |
| 38     | 18  | 112250 | 112462 | lgi 927645      | arginyl endopeptidase [Porphyromonas gingivalis]  | 71    | 50      | 213    |
| 39     | 3   | 1246   | 4431   | lpir S0941 S094 | lspolIE protein - Bacillus subtilis   | 71    | 49      | 3186   |
| 53     | 14  | 115770 | 114760 | lgi 142611      | branched chain alpha-keto acid dehydrogenase E1-alpha [Bacillus subtilis]                           | 71    | 58      | 1011   |
| 54     | 11  | 13461  | 12625  | lgi 143014      | lnt repressor [Bacillus subtilis]   | 71    | 46      | 837    |

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| ID     | ID  | (nt)   | (nt)   | accession  |   | (nt)  | (nt)    | (nt)   |
| 57     | 7   | 7152   | 5860   | gi 508175  | EEIC domain of PTS-dependent Gat transport and phosphorylation Escherichia coli   | 71    | 48      | 1293   |
| 57     | 18  | 113897 | 14334  | gi 1063247 | high homology to flavohemoprotein (Haemoglobin-like protein) of Alcaligenes eutrophus and <i>Saccharomyces cerevisiae</i> [Bacillus subtilis] | 71    | 56      | 438    |
| 62     | 116 | 9831   | 10955  | gi 1303926 | YqIG [Bacillus subtilis]  | 71    | 54      | 1125   |
| 70     | 112 | 8505   | 8966   | gi 147198  | lphnE protein [Escherichia coli]  | 71    | 38      | 462    |
| 86     | 5   | 2394   | 2089   | gi 904205  | hypothetical protein [Bacillus subtilis]  | 71    | 51      | 306    |
| 96     | 7   | 7601   | 8269   | gi 709991  | hypothetical protein [Bacillus subtilis]  | 71    | 49      | 669    |
| 100    | 6   | 4822   | 5931   | gi 1060848 | Opine dehydrogenase [Arthrobacter sp.]  | 71    | 45      | 1110   |
| 103    | 1   | 1062   | 532    | gi 143089  | liep protein [Bacillus subtilis]  | 71    | 41      | 531    |
| 109    | 18  | 115312 | 115695 | gi 413985  | lipa-61d gene product [Bacillus subtilis]   | 71    | 57      | 384    |
| 113    | 1   | 630    | 316    | gi 663254  | probable protein kinase [Saccharomyces cerevisiae]  | 71    | 57      | 315    |
| 114    | 5   | 6598   | 5603   | gi 143156  | membrane bound protein [Bacillus subtilis]  | 71    | 40      | 996    |
| 133    | 2   | 3087   | 1723   | gi 1303913 | Yqhx [Bacillus subtilis]  | 71    | 53      | 1365   |
| 149    | 119 | 63335  | 5895   | gi 529650  | G40P [Bacteriophage SP1]  | 71    | 51      | 441    |
| 154    | 5   | 3635   | 3087   | gi 425488  | repressor protein [Streptococcus sobrinus]  | 71    | 47      | 549    |
| 164    | 11  | 11354  | 11689  | gi 49318   | ORF4 gene product [Bacillus subtilis]   | 71    | 52      | 336    |
| 169    | 5   | 1936   | 2745   | gi 1403403 | unknown [Mycobacterium tuberculosis]  | 71    | 56      | 810    |
| 193    | 2   | 272    | 1234   | gi 1303788 | YqeH [Bacillus subtilis]  | 71    | 49      | 963    |
| 205    | 1   | 1743   | 895    | gi 1215694 | GlnQ [Mycoplasma pneumoniae]  | 71    | 46      | 849    |
| 233    | 4   | 1849   | 2022   | gi 633732  | ORF1 [Campylobacter jejuni]   | 71    | 50      | 174    |
| 237    | 7   | 4501   | 5169   | gi 149384  | HISIE [Lactococcus lactis]  | 71    | 54      | 669    |
| 272    | 4   | 2848   | 2273   | gi 1709993 | hypothetical protein [Bacillus subtilis]  | 71    | 48      | 576    |
| 274    | 2   | 618    | 1496   | gi 143035  | NAD(P)H:glutamyl-transfer RNA reductase [Bacillus subtilis] - acillus   | 71    | 53      | 879    |
| 276    | 5   | 3349   | 2720   | gi 303562  | ORF210 [Escherichia coli]   | 71    | 50      | 630    |
| 287    | 1   | 136    | 660    | gi 310634  | 120 kDa protein [Streptococcus gordonii]  | 71    | 53      | 525    |
| 288    | 6   | 3322   | 2771   | gi 1256625 | putative [Bacillus subtilis]  | 71    | 47      | 552    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop | match           | gene name   | % sim | % ident | length |
|--------|-----|-------|------|-----------------|---|-------|---------|--------|
| ID     | ID  | (nt)  | (nt) | accession       |   | (nt)  | (nt)    | (nt)   |
| 301    | 6   | 3492  | 2461 | gi 467417       | similar to lysine decarboxylase [Bacillus subtilis]                               | 1     | 71      | 57     |
| 306    | 4   | 6607  | 5222 | gi 1256618      | transport protein [Bacillus subtilis]   | 1     | 71      | 56     |
| 307    | 2   | 1536  | 925  | gi 602683       | orfC [Mycoplasma capricolum]  | 1     | 71      | 45     |
| 310    | 5   | 5793  | 5146 | gi 348052       | acetoin utilization protein [Bacillus subtilis]                                   | 1     | 71      | 51     |
| 322    | 1   | 2     | 1303 | gi 1001819      | hypothetical protein [Synechocystis sp.]  | 1     | 71      | 46     |
| 333    | 4   | 4171  | 3995 | gi 467473       | unknown [Bacillus subtilis]   | 1     | 71      | 57     |
| 350    | 2   | 548   | 922  | gi 551879       | ORF 1 [Lactococcus lactis]  | 1     | 71      | 55     |
| 375    | 4   | 1860  | 3071 | gi 467447       | unknown [Bacillus subtilis]   | 1     | 71      | 57     |
| 380    | 5   | 1560  | 2102 | gi 142557       | ATP synthase b subunit [Bacillus megaterium]                                      | 1     | 71      | 43     |
| 414    | 2   | 251   | 637  | gi 580904       | homologous to E.coli rnpA [Bacillus subtilis]                                     | 1     | 71      | 49     |
| 424    | 1   | 335   | 1354 | gi 581305       | L-lactate dehydrogenase [Lactobacillus plantarum]                                 | 1     | 71      | 57     |
| 436    | 4   | 3701  | 3270 | pir PN0501 PN05 | phosphoribosylanthranilate isomerase (EC 5.3.1.24) - Bacillus subtilis (fragment) | 1     | 71      | 66     |
| 482    | 1   | 3     | 1280 | gi 410142       | ORFX18 [Bacillus subtilis]  | 1     | 71      | 49     |
| 525    | 3   | 2272  | 1844 | gi 143370       | phosphoribosylpyrophosphate amidotransferase (PUR-F; EC 2.4.2.14) Bacillus        | 1     | 71      | 56     |
| 529    | 4   | 2739  | 2047 | gi 606150       | ORF f309 [Escherichia coli]   | 1     | 71      | 43     |
| 563    | 1   | 22    | 969  | gi 1237015      | ORF4 [Bacillus subtilis]  | 1     | 71      | 53     |
| 581    | 1   | 1506  | 255  | gi 1301730      | T25G3.2 [Caenorhabditis elegans]  | 1     | 71      | 47     |
| 612    | 2   | 1068  | 913  | gi 153968       | fimbriae Z [Salmonella typhimurium]   | 1     | 71      | 55     |
| 613    | 1   | 1     | 654  | gi 466778       | lysine specific permease [Escherichia coli]                                       | 1     | 71      | 50     |
| 618    | 1   | 1243  | 623  | gi 1146238      | poly(A) polymerase [Bacillus subtilis]  | 1     | 71      | 52     |
| 630    | 1   | 1170  | 586  | gi 1486233      | unknown [Bacillus subtilis]   | 1     | 71      | 53     |
| 691    | 1   | 1126  | 641  | gi 289260       | comE ORF1 [Bacillus subtilis]   | 1     | 71      | 51     |
| 694    | 2   | 149   | 427  | gi 12971        | NADH dehydrogenase subunit V (AA 1-605) [Gallus gallus] ir S10197 S10197          | 1     | 71      | 47     |
| 715    | 2   | 169   | 777  | gi 1303830      | NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain - chicken mitochondrion (SGC1) | 1     | 71      | 53     |
| 746    | 2   | 1473  | 970  | gi 1377843      | YqfL [Bacillus subtilis]  | 1     | 71      | 52     |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop | match      | match gene name  | % sim | % ident | length |
|--------|-----|-------|------|------------|--|-------|---------|--------|
| ID     | ID  | (nt)  | (nt) | accession  |  |       |         | (nt)   |
| 748    | 1   | 1437  | 802  | gi 1405459 | lYneS [Bacillus subtilis]  | 71    | 49      | 636    |
| 753    | 1   | 1018  | 524  | gi 1510389 | [M. jannaschii predicted coding region MJ0296 [Methanococcus jannaschii]             | 71    | 53      | 495    |
| 761    | 1   | 3     | 215  | gi 475972  | lpentafunctional enzyme [Pneumocystis carinii]                                       | 71    | 47      | 213    |
| 783    | 1   | 1203  | 703  | gi 536655  | [ORF YBR214W [Saccharomyces cerevisiae]]   | 71    | 52      | 501    |
| 800    | 3   | 1292  | 987  | gi 1204326 | [tRNA delta(2)-isopentenylpyrophosphate transferase [Haemophilus influenzae]]        | 71    | 48      | 306    |
| 806    | 1   | 116   | 286  | gi 1419075 | lcbiM gene product [Methanobacterium thermoautotrophicum]                            | 71    | 50      | 171    |
| 931    | 1   | 973   | 488  | gi 893358  | lPgsA [Bacillus subtilis]  | 71    | 56      | 486    |
| 1041   | 1   | 2     | 262  | gi 1408507 | lpyrimidine nucleoside transport protein [Bacillus subtilis]                         | 71    | 45      | 261    |
| 1070   | 1   | 2     | 172  | gi 709993  | lhypothetical protein [Bacillus subtilis]  | 71    | 46      | 171    |
| 1176   | 1   | 57    | 365  | gi 151259  | [HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii] pir1A4756lA44756            | 71    | 49      | 309    |
| 1181   | 1   | 366   | 184  | gi 46971   | lepyP gene product [Staphylococcus epidermidis]                                      | 71    | 50      | 183    |
| 1281   | 1   | 3     | 290  | gi 153016  | [ORF 419 protein [Staphylococcus aureus]]  | 71    | 50      | 288    |
| 1348   | 1   | 456   | 229  | gi 602683  | lorfC [Mycoplasma capricolum]  | 71    | 48      | 228    |
| 2002   | 1   | 756   | 379  | gi 1008177 | [ORF YUL046w [Saccharomyces cerevisiae]]   | 71    | 48      | 378    |
| 2119   | 1   | 2     | 217  | gi 1046088 | larginyl-tRNA synthetase [Mycoplasma genitalium]                                     | 71    | 50      | 216    |
| 2418   | 1   | 3     | 320  | gi 1499771 | [M. jannaschii predicted coding region MJ0936 [Methanococcus jannaschii]]            | 71    | 57      | 318    |
| 2961   | 1   | 2     | 187  | gi 312443  | lcarbamoyl-phosphate synthase (glutamine-hydrolysing) [Bacillus albolyticus]         | 71    | 57      | 186    |
| 2999   | 2   | 67    | 306  | gi 710020  | lnitrite reductase (nirB) [Bacillus subtilis]  | 71    | 43      | 240    |
| 3033   | 1   | 2     | 184  | gi 1262335 | lYmaA [Bacillus subtilis]  | 71    | 57      | 183    |
| 3584   | 1   | 3     | 338  | gi 401716  | lbeta-isopropylmalate dehydrogenase [Neurospora crassa]                              | 71    | 55      | 336    |
| 3715   | 2   | 743   | 399  | gi 563952  | lgluconate permease [Bacillus licheniformis]   | 71    | 59      | 345    |
| 3785   | 1   | 770   | 387  | gi 47382   | lacyl-CoA-dehydrogenase [Streptomyces purpurascens]                                  | 71    | 57      | 384    |
| 3875   | 1   | 541   | 272  | gi 1001541 | lhypothetical protein [Synechocystis sp.]  | 71    | 38      | 270    |
| 4135   | 1   | 637   | 320  | gi 142695  | [S-adenosyl-L-methionine:uroporphyrinogen III methyltransferase Bacillus megaterium] | 71    | 52      | 318    |
| 4249   | 1   | 63    | 239  | gi 1205363 | [deoxyribose aldolase [Haemophilus influenzae]]                                      | 71    | 63      | 177    |
| 4508   | 1   | 530   | 267  | gi 1197667 | lvitellogenin [Anolis pulchellus]  | 71    | 46      | 264    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop   | match           | gene name  | % sim | % ident | length |
|--------|-----|-------|--------|-----------------|--|-------|---------|--------|
| ID     | ID  | (nt)  | (nt)   | accession       |  | (nt)  | (nt)    |        |
| 6      | 3   | 1237  | 2721   | lgi 1321788     | larginine ornithine antiporter [Clostridium perfringens]                           | 70    | 54      | 1485   |
| 11     | 11  | 6572  | 7486   | lgi 216854      | P47K [Pseudomonas chlororaphis]  | 70    | 41      | 915    |
| 12     | 1   | 2890  | 1481   | lgi 467330      | replicative DNA helicase [Bacillus subtilis]                                       | 70    | 49      | 1410   |
| 15     | 1   | 1756  | 893    | lgi 451216      | Mannosephosphate Isomerase [Streptococcus mutans]                                  | 70    | 46      | 864    |
| 15     | 2   | 1277  | 1050   | lgi 476092      | Unknown [Bacillus subtilis]  | 70    | 50      | 228    |
| 17     | 2   | 2132  | 1350   | lgi 145402      | Choline dehydrogenase [Escherichia coli]   | 70    | 52      | 783    |
| 21     | 1   | 2     | 925    | lgi 149516      | anthranilate synthase alpha subunit [Lactococcus lactis] pir S35124 S35124         | 70    | 50      | 924    |
|        |     |       |        |                 | anthranilate synthase (EC 4.1.3.27) alpha chain - actococcus lactis subsp. lactis  |       |         |        |
| 25     | 7   | 5580  | 6251   | lgi 1389549     | ORF3 [Bacillus subtilis]   | 70    | 52      | 672    |
| 33     | 6   | 6071  | 7423   | lgi 1303875     | YqhB [Bacillus subtilis]   | 70    | 51      | 1353   |
| 36     | 2   | 959   | 1594   | lgi 500755      | 1-methyl purine glycosylase [Mus musculus]   | 70    | 47      | 636    |
| 38     | 8   | 4901  | 5860   | lgi 1498507     | Pyrimidine nucleoside transport protein [Bacillus subtilis]                        | 70    | 44      | 960    |
| 44     | 8   | 5312  | 5989   | lgi 1006620     | Hypothetical protein [Synechocystis sp.]   | 70    | 49      | 678    |
| 46     | 10  | 8950  | 110020 | lgi 1403126     | IczD gene product [Alcaligenes eutrophus]  | 70    | 45      | 1071   |
| 52     | 2   | 2727  | 1900   | lgi 1486247     | Unknown [Bacillus subtilis]  | 70    | 53      | 828    |
| 52     | 6   | 4048  | 4656   | lgi 244501      | esterase II=carboxylesterase (EC 3.1.1.1) [Pseudomonas fluorescens, epide, 218 aa] |       |         |        |
| 56     | 8   | 8460  | 9962   | lgi 1339951     | Small subunit of NADH-dependent glutamate synthase [Plectonema boryanum]           | 70    | 51      | 1503   |
| 62     | 1   | 48    | 290    | lgi 142702      | Competence protein 2 [Bacillus subtilis]   | 70    | 47      | 243    |
| 64     | 1   | 1080  | 541    | lgi 1204377     | Imolybdopterin biosynthesis protein [Haemophilus influenzae]                       | 70    | 47      | 540    |
| 70     | 5   | 5139  | 3595   | lgi 1204834     | 12',3'-cyclic-nucleotide 2'-phosphodiesterase [Haemophilus influenzae]             | 70    | 47      | 1545   |
| 91     | 4   | 7793  | 5466   | lgi 886471      | l-methionine synthase [Catharanthus roseus]  | 70    | 56      | 2328   |
| 96     | 5   | 8754  | 7255   | pir B39096 B390 | alkaline phosphatase (EC 3.1.3.1) III precursor - Bacillus subtilis                | 70    | 54      | 1500   |
| 110    | 2   | 767   | 1300   | lgi 145294      | adenine phosphoribosyl-transferase [Escherichia coli]                              | 70    | 51      | 534    |
| 116    | 6   | 7026  | 7976   | lgi 143607      | sporulation protein [Bacillus subtilis]  | 70    | 50      | 951    |
| 121    | 8   | 6401  | 6988   | lgi 1107528     | ttg start [Campylobacter coli]   | 70    | 45      | 588    |
| 131    | 8   | 6842  | 7936   | lgi 1150454     | prolidase PepQ [Lactobacillus delbrueckii]   | 70    | 48      | 1095   |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF ID | Start (nt) | Stop (nt) | match accession | match gene name | % sim   | % ident | length (nt) |
|--------|--------|------------|-----------|-----------------|-----------------|---|---------|-------------|
| 1      | 135    | 1          | 2         | 1489            | gi 311309       | putative membrane-bound protein with four times repetition of ro-Ser-Ala at the N-terminus; function unknown [Alcaligenes utrophus] |         |             |
|        | 138    | 3          | 418       | 714             | gi 904181       | hypothetical protein [Bacillus subtilis]  |         |             |
|        | 164    | 8          | 9344      | 9874            | gi 49315        | ORF1 gene product [Bacillus subtilis]   |         |             |
|        | 164    | 16         | 115626    | 16618           | gi 1205212      | hypothetical protein (GB:D10483_18) [Haemophilus influenzae]  |         |             |
|        | 205    | 2          | 2735      | 1803            | gi 1215695      | peptide transport system protein SapF homolog; SapF homolog [Mycoplasma pneumoniae]   |         |             |
|        | 209    | 3          | 910       | 1386            | gi 1204665      | hypothetical protein (GB:XT3124_26) [Haemophilus influenzae]  |         |             |
|        | 246    | 3          | 340       | 756             | gi 215098       | hypothetical protein (Bacteriophage 154a)   |         |             |
|        | 263    | 7          | 7876      | 6749            | gi 142540       | aspartokinase II [Bacillus sp.]   |         |             |
|        | 268    | 3          | 3212      | 4117            | gi 1340128      | ORF1 [Staphylococcus aureus]  |         |             |
|        | 302    | 6          | 3201      | 3827            | gi 147782       | truA protein (tgt start) [Escherichia coli]   |         |             |
|        | 302    | 10         | 5879      | 7051            | pir C38530 C385 | queuine tRNA-ribosyltransferase (EC 2.4.2.29) - Escherichia coli  |         |             |
|        | 313    | 1          | 2520      | 1414            | gi 1205934      | aminopeptidase a/i [Haemophilus influenzae]   |         |             |
|        | 355    | 2          | 379       | 669             | gi 1070013      | protein-dependent [Bacillus subtilis]   |         |             |
|        | 403    | 1          | 1255      | 629             | gi 733147       | GumF [Xanthomonas campestris]   |         |             |
|        | 444    | 10         | 8770      | 9273            | gi 1204752      | high affinity ribose transport protein [Haemophilus influenzae]   |         |             |
|        | 449    | 1          | 2         | 1243            | gi 619724       | MgtE [Bacillus firmus]  |         |             |
|        | 472    | 1          | 637       | 320             | gi 1727145      | open reading frame; putative [Bacillus amyloliquefaciens] pir B29091 B29091   |         |             |
|        | 480    | 2          | 727       | 1608            | gi 142560       | hypothetical protein (bglA region) - Bacillus myloliquefaciens (fragment)   |         |             |
|        | 524    | 1          | 2         | 307             | gi 602292       | ATP synthase gamma subunit [Bacillus megaterium]  |         |             |
|        | 525    | 1          | 823       | 413             | gi 143372       | RCH2 protein [Brassica napus]   |         |             |
|        | 565    | 4          | 3625      | 2552            | gi 881434       | ORF [Bacillus subtilis]   |         |             |
|        | 607    | 4          | 829       | 1284            | gi 1511524      | hypothetical protein (SP:SP37002) [Methanococcus jannaschii]  |         |             |
|        | 633    | 1          | 1383      | 703             | gi 431231       | uracil permease [Bacillus caldolyticus]   |         |             |
|        | 646    | 3          | 1683      | 1309            | gi 467340       | unknown [Bacillus subtilis]   |         |             |
|        | 663    | 1          | 830       | 417             | gi 1303873      | YggZ [Bacillus subtilis]  |         |             |

S. aureus - Putative coding regions of novel proteins similar to known proteins

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|--------|-----|-------|------|------------|---|-------|---------|--------|
| ID     | ID  | (nt)  | (nt) | accession  |   | (nt)  | (nt)    |        |
| 681    | 1   | 1488  | 781  | gi 1001678 | hypothetical protein [Synechocystis sp.]  | 1     | 70      | 53     |
| 708    | 1   | 1     | 2    | 448        | sp P33940 YOJH_ HYPOTHETICAL 54.3 KD PROTEIN IN ECO-ALKB INTERGENIC REGION.   | 1     | 70      | 51     |
| 725    | 1   | 1     | 51   | 722        | gi 1001644 hypothetical protein [Synechocystis sp.]   | 1     | 70      | 48     |
| 776    | 1   | 1     | 1371 | 787        | gi 145165 putative [Escherichia coli]   | 1     | 70      | 47     |
| 834    | 1   | 1     | 250  | 783        | gi 552971 NADH dehydrogenase (ndhF) [Vicia faba]  | 1     | 70      | 47     |
| 865    | 2   | 1     | 1585 | 1379       | gi 1204636 ATP-dependent helicase [Haemophilus influenzae]  | 1     | 70      | 45     |
| 894    | 1   | 1     | 535  | 269        | gi 467364 tDNA binding protein (probale) [Bacillus subtilis]  | 1     | 70      | 41     |
| 919    | 1   | 1     | 3    | 317        | gi 1314847 CinA [Bacillus subtilis]   | 1     | 70      | 40     |
| 944    | 1   | 1     | 3    | 572        | gi 1709991 hypothetical protein [Bacillus subtilis]   | 1     | 70      | 44     |
| 988    | 1   | 2     | 772  | 605        | gi 142441 ORF 3; putative [Bacillus subtilis]   | 1     | 70      | 50     |
| 1055   | 1   | 1     | 3    | 335        | gi 529755 lspec [Streptococcus Pyogenes]  | 1     | 70      | 37     |
| 1093   | 1   | 1     | 2    | 904        | gi 853754 ABC transporter [Bacillus subtilis]   | 1     | 70      | 49     |
| 1109   | 1   | 1     | 2    | 310        | gi 1001827 hypothetical protein [synechocystis sp.]   | 1     | 70      | 42     |
| 1220   | 1   | 1     | 468  | 235        | pir S223416 S234 lepiB protein - Staphylococcus epidermidis   | 1     | 70      | 309    |
| 1279   | 1   | 1     | 73   | 348        | gi 153015 FemA protein [Staphylococcus aureus]  | 1     | 70      | 47     |
| 1336   | 1   | 1     | 195  | 542        | sp P31776 PBPA_ PENICILLIN-BINDING PROTEIN 1A (PBP-1A) (PENICILLIN-BINDING PROTEIN A).  | 1     | 70      | 50     |
| 1537   | 1   | 2     | 232  | 402        | gi 1146181 putative [Bacillus subtilis]   | 1     | 70      | 50     |
| 1574   | 1   | 1     | 451  | 272        | gi 219630 endothelin-A receptor [Homo sapiens]  | 1     | 70      | 47     |
| 1640   | 1   | 1     | 690  | 346        | gi 1146243 122.4% identity with Escherichia coli DNA-damage inducible protein ...; putative [Bacillus subtilis]                       | 1     | 70      | 46     |
| 2504   | 1   | 1     | 2    | 286        | gi 496119 transmembrane protein [Lactococcus lactis]  | 1     | 70      | 51     |
| 3061   | 1   | 1     | 564  | 301        | gi 508175 EIIC domain of PTS-dependent Gat transport and phosphorylation Escherichia coli   | 1     | 70      | 44     |
| 3128   | 1   | 1     | 2    | 199        | gi 1340096 unknown [Mycobacterium tuberculosis]   | 1     | 70      | 51     |
| 3218   | 1   | 1     | 3    | 488        | gi 515938 glutamate synthase (ferredoxin) [Synechocystis sp.] pir S46957 S46957 putative [ferredoxin] (EC 1.4.7.1) - ynechocystis sp. | 1     | 70      | 50     |
| 3323   | 1   | 1     | 794  | 399        | gi 1154891 ATP binding protein [Phormidium laminosum]   | 1     | 70      | 52     |
| 3679   | 1   | 1     | 599  | 399        | gi 529385 chromosome condensation protein [Caenorhabditis elegans]  | 1     | 70      | 30     |

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|--------|-----|-------|-------|-------------|--|-------|---------|--------|
| ID     | ID  | (nt)  | (nt)  | accession   |  | (nt)  | (nt)    |        |
| 3841   | 1   | 706   | 1398  | Igi 1208965 | hypothetical 23.3 kd protein [Escherichia coli]  | 70    | 47      | 309    |
| 3929   | 1   | 1     | 3     | Igi 401     | Igi 149435<br>putative [Lactococcus lactis]  | 70    | 49      | 399    |
| 4044   | 1   | 1     | 595   | Igi 602031  | similar to trimethylamine DH [Mycoplasma capricolum] piri S49950/S49950<br>probable trimethylamine dehydrogenase (EC 5.99.7) - Mycoplasma capricolum | 70    | 40      | 222    |
|        |     |       |       |             | (SGC3) (fragment)  |       |         |        |
| 4329   | 1   | 1     | 558   | Igi 280     | Igi 1339951<br>small subunit of NADH-dependent glutamate synthase [Plectonema boryanum]  | 70    | 49      | 279    |
| 4422   | 1   | 1     | 576   | Igi 289     | Igi 296464<br>ATPase [Lactococcus lactis]  | 70    | 57      | 288    |
| 4647   | 1   | 1     | 361   | Igi 200     | Igi 166412<br> NADH-glutamate synthase [Medicago sativa]   | 70    | 59      | 162    |
| 16     | 8   | 1     | 7571  | Igi 9031    | Igi 1499620<br> M. jannaschii predicted coding region MJ0798 [Methanococcus jannaschii]  | 69    | 44      | 1461   |
| 16     | 9   | 1     | 9080  | Igi 10033   | Igi 1353197<br>lthioredoxin reductase [Eubacterium acidaminophilum]  | 69    | 54      | 954    |
| 30     | 1   | 1     | 1452  | Igi 727     | Igi 1204910<br>hypothetical protein (GB:U14003_302) [Haemophilus influenzae]   | 69    | 52      | 726    |
| 38     | 4   | 1     | 1023  | Igi 1298    | Igi 407773<br>ldevA gene product [Anabaena sp.]  | 69    | 41      | 276    |
| 44     | 9   | 1     | 5987  | Igi 6595    | Igi 1205920<br> molybdate uptake system hydrophilic membrane-bound protein [Haemophilus influenzae]  | 69    | 45      | 609    |
| 62     | 15  | 1     | 9104  | Igi 9475    | Igi 386178<br>lunkown [Bacillus subtilis]  | 69    | 44      | 372    |
| 66     | 4   | 1     | 2402  | Igi 2803    | Igi 1303893<br> Yqhl [Bacillus subtilis]   | 69    | 51      | 402    |
| 67     | 15  | 1     | 14124 | Igi 13627   | Igi 149647<br> ORFZ [Listeria monocytogenes]   | 69    | 37      | 498    |
| 67     | 17  | 1     | 14053 | Igi 14382   | Igi 305002<br> ORF_f356 [Escherichia coli]   | 69    | 49      | 330    |
| 67     | 19  | 1     | 15130 | Igi 15807   | Igi 1109684<br> Prov [Bacillus subtilis]   | 69    | 45      | 678    |
| 78     | 3   | 1     | 1447  | Igi 2124    | Igi 1256633<br> putative [Bacillus subtilis]   | 69    | 53      | 678    |
| 78     | 4   | 1     | 4513  | Igi 3725    | Igi 1303958<br> YqjG [Bacillus subtilis]   | 69    | 32      | 789    |
| 85     | 4   | 1     | 4521  | Igi 4213    | Igi E29326/E293<br>hypothetical protein (pur operon) - Bacillus subtilis   | 69    | 32      | 309    |
| 86     | 6   | 1     | 3253  | Igi 2654    | Igi 973332<br> OrfC [Bacillus subtilis]  | 69    | 50      | 600    |
| 95     | 1   | 1     | 96    | Igi 710     | Igi 786468<br> 4A11 antigen, sperm tail membrane antigen=putative sucrose-specific   | 69    | 43      | 615    |
|        |     |       |       |             | phosphotransferase enzyme II homolog [mice, testis, Peptide Partial, 72 aa]  |       |         |        |
| 100    | 7   | 1     | 6023  | Igi 7426    | Igi 1205355<br> Na+/H+ antiporter [Haemophilus influenzae]   | 69    | 39      | 1404   |
| 102    | 2   | 1     | 2678  | Igi 1650    | Igi 561690<br> Sialoglucoprotease [Pasteurella haemolytica]  | 69    | 47      | 1029   |
| 103    | 8   | 1     | 12241 | Igi 8537    | Igi 1009366<br> Respiratory nitrate reductase [Bacillus subtilis]  | 69    | 54      | 3705   |
| 103    | 11  | 1     | 14987 | Igi 12552   | Igi 710020<br> Nitrite reductase (nirB) [Bacillus subtilis]  | 69    | 51      | 2436   |

*S. aureus* - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop   | match           | gene name   | % sim | % ident | length |
|--------|-----|--------|--------|-----------------|---|-------|---------|--------|
| ID     | ID  | (nt)   | (nt)   | accession       |   | (nt)  | (nt)    | (nt)   |
| 112    | 111 | 8708   | 10168  | gi 154411       | hexosephosphate transport protein [Salmonella typhimurium]<br>  pir D41853 D41853 hexose phosphate transport system protein uhpt -<br>  almonella typhimurium | 69    | 51      | 1461   |
| 112    | 116 | 116644 | 17414  | gi 1204435      | lpyruvate formate-lyase activating enzyme [Haemophilus influenzae]  | 69    | 50      | 771    |
| 113    | 2   | 33     | 953    | gi 290509       | l0307 [Escherichia coli]  | 69    | 43      | 921    |
| 114    | 2   | 1537   | 1058   | pir A42771 A427 | lreticulocyte-binding protein 1 - Plasmodium vivax  | 69    | 39      | 480    |
| 121    | 6   | 4309   | 5310   | gi 1154633      | NrdF [Bacillus subtilis]  | 69    | 53      | 1002   |
| 125    | 2   | 267    | 854    | gi 413931       | lipa-7d gene product [Bacillus subtilis]  | 69    | 43      | 588    |
| 149    | 127 | 10666  | 110400 | pir S28089 S280 | lhypothetical protein A - yeast (zygosaccharomyces bisporus) plasmid psB3   | 69    | 39      | 267    |
| 161    | 1   | 1598   | 813    | gi 1205538      | lhypothetical protein [GB:U14003_302] [Haemophilus influenzae]  | 69    | 47      | 786    |
| 165    | 4   | 2222   | 4633   | gi 140054       | lphenylalanyl-tRNA synthetase beta subunit (AA 1-804) [Bacillus subtilis]   | 69    | 52      | 2412   |
| 169    | 3   | 1210   | 1761   | gi 296031       | lelongation factor Ts [Spirulina platensis]   | 69    | 45      | 552    |
| 175    | 112 | 8686   | 8339   | gi 1732682      | FimE protein [Escherichia coli]   | 69    | 69      | 348    |
| 190    | 2   | 484    | 1671   | sp P17731 HIS8  | lHISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9) (IMIDAZOLE ACETOL-<br>  PHOSPHATE TRANSAMINASE).  | 69    | 48      | 1188   |
| 206    | 1   | 5551   | 2777   | gi 41750        | lhsdR protein (AA 1-1033) [Escherichia coli]  | 69    | 49      | 2775   |
| 206    | 4   | 6038   | 5796   | gi 1256135      | YbbF [Bacillus subtilis]  | 69    | 48      | 243    |
| 249    | 1   | 636    | 319    | gi 1405456      | YneP [Bacillus subtilis]  | 69    | 50      | 318    |
| 302    | 8   | 4820   | 5776   | gi 1101768      | lhypothetical protein [Synechocystis sp.]   | 69    | 48      | 957    |
| 324    | 2   | 7384   | 3893   | gi 1256798      | lpyruvate carboxylase [Rhizobium etli]  | 69    | 53      | 3492   |
| 351    | 3   | 2098   | 1808   | gi 1491664      | T04H1.4 [Caenorhabditis elegans]  | 69    | 30      | 291    |
| 369    | 3   | 2075   | 2305   | gi 336458       | ORF [Balaenoptera acutorostrata]  | 69    | 61      | 231    |
| 392    | 3   | 1999   | 2424   | gi 556015       | ORF1 [Bacillus subtilis]  | 69    | 45      | 426    |
| 410    | 1   | 87     | 779    | gi 155611       | lphosphoglyceromutase [Zymomonas mobilis]   | 69    | 58      | 693    |
| 421    | 1   | 2085   | 1129   | gi 1276985      | larginase [Bacillus caldovelox]   | 69    | 54      | 957    |
| 444    | 8   | 6713   | 7741   | gi 1221782      | lpurine synthesis repressor [Haemophilus influenzae]  | 69    | 40      | 1029   |
| 453    | 1   | 828    | 415    | gi 1122738      | lunknown [Bacillus subtilis]  | 69    | 57      | 414    |
| 469    | 2   | 3286   | 2246   | gi 1458228      | lmutY homolog [Homo sapiens]  | 69    | 44      | 1041   |

*S. aureus* - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop | match       | gene name   | % sim | % ident | length |
|--------|-----|-------|------|-------------|---|-------|---------|--------|
| ID     | ID  | (nt)  | (nt) | accession   |   | (nt)  | (nt)    | (nt)   |
| 509    | 3   | 1730  | 1371 | lgi 49224   | IURF 4 [Synechococcus sp.]  | 69    | 39      | 360    |
| 520    | 5   | 3023  | 2823 | lgi 726427  | similar to D. melanogaster MST101-2 protein (PIR:S34154) Caenorhabditis elegans]  | 69    | 39      | 201    |
| 531    | 1   | 26    | 760  | lgi 509672  | repressor protein [Bacteriophage Tuc2009]   | 69    | 33      | 735    |
| 589    | 1   | 107   | 253  | lgi 169101  | 117.9 kDa heat shock protein (hsp17.9) [Pisum sativum]  | 69    | 52      | 147    |
| 594    | 2   | 597   | 1391 | lgi 142783  | lDNA photolyase [Bacillus firmus]   | 69    | 48      | 795    |
| 604    | 4   | 2476  | 2114 | lgi 413930  | lipa-6d gene product [Bacillus subtilis]  | 69    | 45      | 363    |
| 607    | 1   | 2     | 313  | lgi 1236103 | lW08D2.3 [Caenorhabditis elegans]   | 69    | 47      | 312    |
| 607    | 2   | 590   | 312  | lgi 536715  | lORF YBR275c [Saccharomyces cerevisiae]   | 69    | 39      | 279    |
| 734    | 1   | 864   | 433  | lgi 467327  | lunknown [Bacillus subtilis]  | 69    | 44      | 432    |
| 759    | 1   | 3     | 338  | lgi 1009367 | lRespiratory nitrate reductase [Bacillus subtilis]  | 69    | 50      | 336    |
| 761    | 2   | 392   | 586  | lgi 3508    | lLeucyl-tRNA synthetase (cytoplasmic) [Saccharomyces cerevisiae] lORF YPL160w [Saccharomyces cerevisiae]                            | 69    | 46      | 195    |
| 802    | 1   | 72    | 1013 | lgi 143044  | lferrochelatase [Bacillus subtilis]   | 69    | 55      | 942    |
| 816    | 1   | 2573  | 1368 | lgi 1510268 | lrestriction modification system S subunit [Methanococcus jannaschii]   | 69    | 45      | 1206   |
| 838    | 2   | 133   | 387  | lgi 1255371 | lcoded for by C. elegans cDNA yk34a9.5; coded for by C. elegans cDNA yk34a9.3; Similar to guanylate kinase [caenorhabditis elegans] | 69    | 46      | 255    |
| 851    | 2   | 745   | 1005 | lgi 288998  | lsecA gene product [Antithamnion sp.]   | 69    | 39      | 261    |
| 867    | 1   | 535   | 269  | lgi 1070014 | lprotein-dependent [Bacillus subtilis]  | 69    | 47      | 267    |
| 995    | 1   | 954   | 478  | lgi 1205569 | ltranscription elongation factor [Haemophilus influenzae]   | 69    | 53      | 477    |
| 999    | 1   | 1009  | 506  | lgi 899254  | lpredicted trithorax protein [Drosophila virilis]   | 69    | 21      | 504    |
| 1127   | 1   | 1315  | 659  | lgi 1205434 | lH. influenzae predicted coding region H11191 [Haemophilus influenzae]  | 69    | 56      | 657    |
| 1138   | 1   | 248   | 460  | lgi 1510646 | lM. jannaschii predicted coding region MJ0568 [Methanococcus jannaschii]  | 69    | 48      | 213    |
| 2928   | 1   | 3     | 401  | lgi 290503  | lglutamate permease [Escherichia coli]  | 69    | 41      | 399    |
| 3090   | 1   | 444   | 223  | lgi 1204987 | lDNA polymerase III, alpha chain [Haemophilus influenzae]   | 69    | 36      | 222    |
| 3817   | 1   | 2     | 400  | lgi 1983199 | lpeptide-synthetase [Amycolatopsis mediterranei]  | 69    | 45      | 399    |
| 3833   | 1   | 667   | 335  | lgi 1524193 | lunknown [Mycobacterium tuberculosis]   | 69    | 46      | 333    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF ID | Start (nt) | Stop (nt) | match accession | match gene name  |
|--------|--------|------------|-----------|-----------------|--|
| 4079   | 1      | 747        | 400       | gi 546918       | orf3' of comK [Bacillus subtilis, E26, Peptide Partial, 140 aa]<br>  pir S43612 S43612 hypothetical protein Y - Bacillus subtilis<br>  sp P40398 YHxD_BACSU HYPOTHETICAL PROTEIN IN COMK 3' REGION (ORF Y-<br>FRAGMENT). |
| 4115   | 2      | 215        | 400       | gi 517205       | 167 kDa Myosin-crossreactive streptococcal antigen [Streptococcus yogenes]<br>  69   59   186  |
| 4139   | 1      | 1          | 333       | gi 1208451      | Hypothetical protein [Synechocystis sp.]   |
| 4258   | 1      | 457        | 230       | gi 496158       | restriction-modification enzyme subunit M1 [Mycoplasma pulmonis]<br>  pir S49395 S49395 HsdM1 protein - Mycoplasma pulmonis (SGC3)   |
| 4317   | 1      | 90         | 374       | gi 413967       | lipa-43d gene product [Bacillus subtilis]  |
| 4465   | 1      | 3          | 293       | gi 396296       | similar to phosphotransferase system enzyme II [Escherichia coli]<br>  sp P32672 PTWC_ECOLI PTS SYSTEM, FRUCTOSE-LIKE-2 IIC COMPONENT<br>  PHOSPHOTRANSFERASE ENZYME II, C COMPONENT.                                    |
| 3      | 1      | 2302       | 1193      | gi 1109685      | Prow [Bacillus subtilis]   |
| 15     | 4      | 2592       | 2074      | gi 807973       | lunknown [Saccharomyces cerevisiae]  |
| 31     | 8      | 6328       | 8772      | gi 290642       | ATPase (Enterococcus hirae)  |
| 40     | 2      | 1115       | 750       | gi 606342       | ORF_0622; reading frame open far upstream of start; possible rameshshift,<br>  linking to previous ORF [Escherichia coli]  |
| 46     | 9      | 6886       | 8415      | gi 155276       | aldehyde dehydrogenase [Vibrio cholerae]   |
| 48     | 3      | 3643       | 3404      | gi 2855608      | 241k polyprotein [Apple stem grooving virus]   |
| 48     | 4      | 3536       | 4132      | gi 1045937      | M. genitalium predicted coding region MG246 [Mycoplasma genitalium]  |
| 53     | 10     | 11671      | 10685     | gi 1303952      | YqjA [Bacillus subtilis]   |
| 70     | 9      | 7346       | 8155      | gi 147198       | IphnE protein [Escherichia coli]   |
| 89     | 4      | 1899       | 2966      | gi 145173       | 135 kDa protein [Escherichia coli]   |
| 108    | 1      | 2187       | 1150      | gi 38722        | precursor (aa -20 to 381) [Acinetobacter calcoaceticus] ir[A29277 A29277]<br>  aldose 1-epimerase (EC 5.1.3.3) - Acinetobacter lcoaceticus   |
| 112    | 5      | 2666       | 3622      | gi 153724       | MalC [Streptococcus pneumoniae]  |
| 116    | 7      | 7865       | 8638      | gi 143608       | sporulation protein [Bacillus subtilis]  |
| 118    | 3      | 2484       | 3698      | gi 1303805      | YqeR [Bacillus subtilis]   |
| 120    | 2      | 1424       | 1594      | sp P38038 CYSJ_ | SULFITE REDUCTASE (NADPH) FLAVOPROTEIN ALPHA-COMPONENT (EC 1.8.1.2) (SIR-<br>  FP).  |
| 129    | 1      | 1          | 1011      | gi 396307       | argininosuccinate lyase [Escherichia coli]   |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop   | match     | match gene name | % sim           | % ident  | length |
|--------|-----|-------|--------|-----------|-----------------|-----------------|--|--------|
| ID     | ID  | (nt)  | (nt)   | accession | (nt)            |                 |  | (nt)   |
| 132    | 1   | 3     | 1867   | 1         | 2739            | gi 216267       | ORF2 [Bacillus megaterium]   | 1      |
| 134    | 1   | 2     | 848    | 1         | 1012            | gi 147545       | lDNA recombinase [Escherichia coli]                                      | 1      |
| 141    | 1   | 2     | 372    | 1         | 614             | gi 872116       | lsti (stress inducible protein) [Glycine max]                            | 1      |
| 149    | 1   | 7     | 2454   | 1         | 2260            | gi 145774       | hsp70 protein (dnaK gene) [Escherichia coli]                             | 1      |
| 155    | 1   | 2     | 1776   | 1         | 1534            | gi 216583       | lORF1 [Escherichia coli]   | 1      |
| 158    | 1   | 3     | 1826   | 1         | 3289            | sp P33940 YQJH  | HYPOTHETICAL 54.3 KD PROTEIN IN ECO-ALKB INTERGENIC REGION.              | 1      |
| 169    | 1   | 6     | 2749   | 1         | 3318            | gi 1403402      | lunknown [Mycobacterium tuberculosis]                                    | 1      |
| 175    | 1   | 10    | 9158   | 1         | 7365            | gi 1072395      | phaA gene product [Rhizobium meliloti]                                   | 1      |
| 188    | 1   | 7     | 4184   | 1         | 5434            | gi 1173843      | 13-ketoacyl-ACP synthase II [Vibrio harveyi]                             | 1      |
| 189    | 1   | 3     | 907    | 1         | 1665            | gi 467383       | lDNA binding protein (probable) [Bacillus subtilis]                      | 1      |
| 206    | 1   | 5     | 7683   | 1         | 6709            | gi 1256138      | YbbI [Bacillus subtilis]   | 1      |
| 206    | 1   | 8     | 110425 | 1         | 12176           | gi 452687       | lpyruvate decarboxylase [Saccharomyces cerevisiae]                       | 1      |
| 212    | 1   | 8     | 3421   | 1         | 3648            | gi 1369941      | c1 gene product [Bacteriophage B1]                                       | 1      |
| 214    | 1   | 8     | 5457   | 1         | 6482            | gi 1420467      | ORF YOR196c [Saccharomyces cerevisiae]                                   | 1      |
| 237    | 1   | 4     | 2507   | 1         | 3088            | gi 149381       | HisH [Lactococcus lactis]  | 1      |
| 243    | 1   | 5     | 5540   | 1         | 4542            | gi 1235684      | lmevalonate pyrophosphate decarboxylase [Saccharomyces cerevisiae]       | 1      |
| 262    | 1   | 1     | 3      | 1         | 164             | gi 150974       | l4-oxalocrotonate tautomerase [Pseudomonas putida]                       | 1      |
| 262    | 1   | 2     | 1984   | 1         | 1118            | gi 1147744      | PSR [Enterococcus hirae]   | 1      |
| 276    | 1   | 6     | 3702   | 1         | 3139            | sp P30750 ABC_E | lATP-BINDING PROTEIN ABC (FRAGMENT).                                     | 1      |
| 306    | 1   | 6     | 6345   | 1         | 5725            | gi 1256617      | ladenine phosphoribosyltransferase [Bacillus subtilis]                   | 1      |
| 333    | 1   | 3     | 4599   | 1         | 3850            | gi 467473       | lunknown [Bacillus subtilis]   | 1      |
| 365    | 1   | 6     | 5017   | 1         | 4838            | gi 1130643      | T22B3.3 [Caenorhabditis elegans]   | 1      |
| 376    | 1   | 2     | 549    | 1         | 1646            | gi 1277026      | DAPA aminotransferase [Bacillus subtilis]                                | 1      |
| 405    | 1   | 1     | 1741   | 1         | 872             | gi 1303917      | YqiB [Bacillus subtilis]   | 1      |
| 406    | 1   | 2     | 853    | 1         | 539             | gi 1511513      | ABC transporter, probable ATP-binding subunit [Methanococcus jannaschii] | 1      |
| 426    | 1   | 6     | 3558   | 1         | 3391            | gi 624632       | GltL [Escherichia coli]  | 1      |
| 438    | 1   | 1     | 108    | 1         | 329             | gi 146923       | lNitrogenase reductase [Escherichia coli]                                | 1      |

## S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop | match accession | match gene name   | % sim | % ident | length |
|--------|-----|-------|------|-----------------|---|-------|---------|--------|
| ID     | ID  | (nt)  | (nt) |                 |   |       |         | (nt)   |
| 443    | 1   | 476   | 1240 | lgi 535810      | lippuricase [Campylobacter jejuni]  | 68    | 42      | 237    |
| 443    | 2   | 518   | 1015 | lgi 1204742     | [H. influenzae predicted coding region HI0491 [Haemophilus influenzae]  | 68    | 48      | 498    |
| 443    | 5   | 4447  | 3779 | lgi 809660      | deoxyribose-phosphate aldolase [Bacillus subtilis] pir S49455 S49455  | 68    | 55      | 669    |
| 476    | 2   | 240   | 1184 | lgi 971345      | lunknown, similar to E.coli cardiolipin synthase [Bacillus subtilis] sp P45860 YWE_BACSU HYPOTHETICAL 58.2 PROTEIN IN NARI-ACDA NTERGENIC REGION.                 | 68    | 45      | 945    |
| 486    | 2   | 1876  | 1046 | lgi 147328      | ltransport protein [Escherichia coli]   | 68    | 41      | 831    |
| 517    | 3   | 1764  | 2084 | lgi 1523809     | lorf2 [Bacteriophage A2]  | 68    | 64      | 321    |
| 572    | 1   | 2     | 571  | lsp P39237 Y05L | [HYPOTHETICAL 6.8 KD PROTEIN IN NRDC-TK INTERGENIC REGION.  | 68    | 47      | 570    |
| 646    | 1   | 914   | 459  | lgi 413982      | lipa-5Br gene product [Bacillus subtilis]   | 68    | 52      | 456    |
| 659    | 3   | 1668  | 1901 | lgi 1107541     | lC33D9.8 [Caenorhabditis elegans]   | 68    | 36      | 234    |
| 864    | 5   | 1510  | 1716 | lgi 145774      | lhsp70 protein (dnaK gene) [Escherichia coli]   | 68    | 48      | 207    |
| 920    | 1   | 860   | 432  | lgi 1510416     | [hypothetical protein (SP:P31466) [Methanococcus jannaschii]  | 68    | 54      | 429    |
| 952    | 1   | 1096  | 611  | lgi 603456      | lreductase [Leishmania major]   | 68    | 46      | 486    |
| 970    | 1   | 91    | 402  | lgi 1354775     | lpf0S/R [Treponema pallidum]  | 68    | 46      | 312    |
| 1028   | 1   | 1064  | 534  | lgi 410117      | ldiaminopimelate decarboxylase [Bacillus subtilis]  | 68    | 47      | 531    |
| 1029   | 1   | 428   | 216  | lgi 1335714     | [Plasmidium falciparum mRNA for asparagine-rich antigen (clone 17C1) [Plasmidium falciparum]  | 68    | 31      | 213    |
| 1058   | 1   | 692   | 348  | lgi 581649      | lepic gene product [Staphylococcus epidermidis]   | 68    | 46      | 345    |
| 1096   | 2   | 665   | 465  | lgi 143434      | lRho Factor [Bacillus subtilis]   | 68    | 43      | 201    |
| 1308   | 1   | 2     | 694  | lgi 1469939     | lgroup B oligopeptidase PepB [Streptococcus agalactiae]   | 68    | 50      | 693    |
| 1679   | 1   | 2     | 238  | lgi 517205      | l67 kDa Myosin-crossreactive streptococcal antigen [Streptococcus yogenes]  | 68    | 53      | 237    |
| 2039   | 1   | 3     | 383  | lgi 153898      | ltransport protein [Salmonella typhimurium]   | 68    | 51      | 381    |
| 2112   | 1   | 613   | 374  | lgi 64884       | llamin LII [Xenopus laevis]   | 68    | 50      | 240    |
| 2273   | 1   | 793   | 398  | lgi 581648      | lepiB gene product [Staphylococcus epidermidis]   | 68    | 45      | 396    |
| 2948   | 1   | 2     | 385  | lgi 216869      | lbranched-chain amino acid transport carrier [Pseudomonas aeruginosa] pir A38534 A38534 branched-chain amino acid transport protein braZ [Pseudomonas aeruginosa] | 68    | 41      | 384    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop | match      | match gene name   | % sim | % ident | length |
|--------|-----|-------|------|------------|---|-------|---------|--------|
| ID     | ID  | (nt)  | (nt) | accession  |   |       |         | (nt)   |
| 2955   | 1   | 768   | 1400 | gi 904179  | hypothetical protein [Bacillus subtilis]  | 1     | 68      | 49     |
| 2981   | 1   | 572   | 288  | gi 508979  | GTP-binding protein [Bacillus subtilis]   | 1     | 68      | 48     |
| 3014   | 1   | 584   | 294  | gi 1524394 | ORF-2 upstream of gbsAB operon [Bacillus subtilis]  | 1     | 68      | 45     |
| 3082   | 1   | 336   | 169  | gi 1204696 | fructose-permease IIBC component [Haemophilus influenzae]   | 1     | 68      | 53     |
| 3108   | 1   | 103   | 258  | gi 217855  | heat-shock protein [Arabidopsis thaliana]   | 1     | 68      | 48     |
| 3639   | 1   | 919   | 461  | gi 1510490 | nitrate transport permease protein [Methanococcus jannaschii]   | 1     | 68      | 47     |
| 3657   | 1   | 1     | 330  | gi 155369  | PTS enzyme-II fructose [Xanthomonas campestris]   | 1     | 68      | 48     |
| 3823   | 1   | 780   | 391  | gi 603768  | HutI protein, imidazolone-5-propionate hydrolase [Bacillus subtilis]<br>gi 603768 HutI protein, imidazolone-5-propionate hydrolase Bacillus subtilis]                                 | 1     | 68      | 54     |
| 3982   | 1   | 2     | 277  | gi 149435  | putative [Lactococcus lactis]   | 1     | 68      | 47     |
| 4051   | 1   | 1     | 342  | gi 450688  | hsdM gene of EcoprrI gene product [Escherichia coli] pir S38437 S38437 hsdM<br>protein - Escherichia coli pir S09629 S09629 hypothetical protein A -<br>Escherichia coli (SUB 40-520) | 68    | 48      | 342    |
| 4089   | 1   | 12    | 209  | gi 1353678 | heavy-metal transporting P-type ATPase [Proteus mirabilis]  | 1     | 68      | 47     |
| 4143   | 1   | 47    | 187  | gi 603769  | HutU protein, urocanase [Bacillus subtilis]   | 1     | 68      | 55     |
| 4148   | 1   | 2     | 352  | gi 450688  | hsdM gene of EcoprrI gene product [Escherichia coli] pir S38437 S38437 hsdM<br>protein - Escherichia coli pir S09629 S09629 hypothetical protein A -<br>Escherichia coli (SUB 40-520) | 68    | 51      | 351    |
| 4173   | 1   | 2     | 382  | gi 1041097 | Pyruvate Kinase [Bacillus psychrophilus]  | 1     | 68      | 48     |
| 4182   | 1   | 498   | 250  | gi 413968  | lipA-44d gene product [Bacillus subtilis]   | 1     | 68      | 50     |
| 4362   | 2   | 148   | 318  | gi 450688  | hsdM gene of EcoprrI gene product [Escherichia coli] pir S38437 S38437 hsdM<br>protein - Escherichia coli pir S09629 S09629 hypothetical protein A -<br>Escherichia coli (SUB 40-520) | 68    | 44      | 171    |
| 5      | 11  | 9493  | 8300 | gi 143727  | putative [Bacillus subtilis]  | 1     | 67      | 46     |
| 31     | 11  | 10318 | 9833 | gi 216746  | D-lactate dehydrogenase [Lactobacillus plantarum]   | 1     | 67      | 41     |
| 32     | 3   | 1560  | 3155 | gi 1098557 | renal sodium/dicarboxylate cotransporter [Homo sapiens]   | 1     | 67      | 46     |
| 32     | 5   | 4945  | 4145 | gi 1510720 | lphenylate dehydratase [Methanococcus jannaschii]   | 1     | 67      | 51     |
| 36     | 5   | 5350  | 4268 | gi 1146216 | 45% identity with the product of the ORF6 gene from the Erwinia herbicola<br>carotenoid biosynthesis cluster; putative [Bacillus subtilis]  | 67    | 58      | 1083   |
| 44     | 7   | 4492  | 5304 | gi 1006621 | hypothetical protein [Synechocystis sp.]  | 67    | 43      | 813    |

## S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop   | match<br>accession | match<br>gene name  | % sim | % ident | length<br>(nt) |
|--------|-----|--------|--------|--------------------|---|-------|---------|----------------|
| ID     | ID  | (nt)   | (nt)   |                    |   |       |         |                |
| 56     | 7   | 3943   | 8481   | gi 304131          | glutamate synthase large subunit precursor [Azospirillum brasiliense]<br>  pir B46602 B46602 glutamate synthase (NADPH) (EC 1.4.1.13) alpha chain -<br>  Azospirillum brasiliense | 67    | 52      | 4539           |
| 56     | 12  | 113923 | 14678  | gi 1000453         | TreR [Bacillus subtilis]  | 67    | 48      | 756            |
| 62     | 8   | 5092   | 4757   | gi 1113949         | orf3 [Bacillus, C-125, alkali-sensitive mutant 18224, Peptide Mutant, 112<br>aa]  | 67    | 45      | 336            |
| 62     | 10  | 7570   | 6338   | gi 854655          | Na/H antiporter system [Bacillus alcalophilus]  | 67    | 49      | 1233           |
| 99     | 3   | 2119   | 3321   | gi 1204349         | hypothetical protein (GB:GB:D90212_3) [Haemophilus influenzae]  | 67    | 50      | 1203           |
| 102    | 9   | 5695   | 7176   | gi 149432          | putative [Lactococcus lactis]   | 67    | 51      | 1482           |
| 103    | 13  | 114549 | 14049  | gi 1408497         | LP9D gene product [Bacillus subtilis]   | 67    | 48      | 501            |
| 109    | 15  | 114821 | 13982  | gi 413976          | lipa-52r gene product [Bacillus subtilis]   | 67    | 49      | 840            |
| 109    | 17  | 14811  | 15194  | gi 413983          | lipa-59d gene product [Bacillus subtilis]   | 67    | 29      | 384            |
| 121    | 4   | 1713   | 2153   | gi 1262335         | YmaA [Bacillus subtilis]  | 67    | 54      | 441            |
| 122    | 1   | 1      | 1149   | gi 143047          | ORFB [Bacillus subtilis]  | 67    | 35      | 1149           |
| 124    | 5   | 4060   | 3518   | gi 556885          | Unknown [Bacillus subtilis]   | 67    | 47      | 543            |
| 131    | 2   | 4584   | 3589   | gi 1046081         | hypothetical protein (GB:D26185_10) [Mycoplasma genitalium]   | 67    | 30      | 996            |
| 140    | 3   | 2899   | 2297   | gi 146549          | lkdpC [Escherichia coli]  | 67    | 45      | 603            |
| 142    | 4   | 5409   | 4198   | gi 1212775         | GTP cyclohydrolase II [Bacillus amyloliquefaciens]  | 67    | 55      | 1212           |
| 147    | 5   | 2913   | 2374   | gi 1303709         | YrkJ [Bacillus subtilis]  | 67    | 44      | 540            |
| 152    | 8   | 6341   | 6673   | gi 1377841         | Unknown [Bacillus subtilis]   | 67    | 48      | 333            |
| 161    | 4   | 2720   | 3763   | gi 496319          | SphX [Synechococcus sp.]  | 67    | 47      | 1044           |
| 163    | 6   | 1989   | 3428   | gi 595681          | 12-oxoglutarate/malate translocator [Spinacia oleracea]   | 67    | 47      | 1440           |
| 193    | 3   | 1351   | 1626   | gi 1511101         | lshikimate 5-dehydrogenase [Methanococcus jannaschii]   | 67    | 53      | 276            |
| 200    | 2   | 917    | 2179   | gi 142439          | ATP-dependent nuclease [Bacillus subtilis]  | 67    | 48      | 1263           |
| 206    | 110 | 112445 | 12801  | sp P37347 YECD     | HYPOTHETICAL 21.8 KD PROTEIN IN ASPS 5' REGION.   | 67    | 47      | 357            |
| 206    | 111 | 113047 | 114432 | gi 732813          | branched-chain amino acid carrier [Lactobacillus delbrueckii]   | 67    | 46      | 1386           |
| 208    | 2   | 1321   | 809    | gi 10333037        | 1100 kDa heat shock protein (Hsp100) [Leishmania major]   | 67    | 36      | 513            |
| 238    | 3   | 1039   | 2052   | gi 809542          | CbrB protein [Erwinia chrysanthemi]   | 67    | 42      | 1014           |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop | match accession  | match gene name  | % sim | % ident | length |
|--------|-----|-------|------|------------------|--|-------|---------|--------|
| ID     | ID  | (nt)  | (nt) |                  |  | (nt)  | (nt)    |        |
| 246    | 2   | 176   | 367  | lgi 215098       | excisionase [Bacteriophage 154a]   | 1     | 67      | 37     |
| 276    | 2   | 2260  | 1412 | lgi 303560       | lORF271 [Escherichia coli]   | 1     | 67      | 50     |
| 297    | 6   | 2223  | 3056 | lgi 142784       | lCtaA protein [Bacillus firmus]  | 1     | 67      | 46     |
| 307    | 7   | 5220  | 4186 | lgi 1070013      | lprotein-dependent [Bacillus subtilis]   | 1     | 67      | 43     |
| 316    | 1   | 36    | 1028 | lgi 1161061      | ldioxygenase [Methylobacterium extorquens]   | 1     | 67      | 52     |
| 324    | 3   | 5650  | 5030 | lgi 1469784      | lputative cell division protein ftsW [Enterococcus hirae]                                    | 1     | 67      | 49     |
| 336    | 1   | 524   | 264  | lgi 173122       | lurea amidolyase [Saccharomyces cerevisiae]  | 1     | 67      | 45     |
| 360    | 1   | 108   | 1394 | sp P30053 SYH_S  | lHISTIDYL-TRNA SYNTHETASE (EC 6.1.1.21) (HISTIDINE--TRNA LIGASE) (HISRS).                    | 1     | 67      | 47     |
| 364    | 3   | 4890  | 3592 | lgi 151259       | lHMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii] pir A44756 A44756                   | 1     | 67      | 46     |
| 365    | 3   | 2940  | 2113 | lgi 1296823      | lhydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii] pir A44756 A44756 | 1     | 67      | 46     |
| 367    | 2   | 325   | 918  | lgi 1039479      | lorf2 gene product [Lactobacillus helveticus]  | 1     | 67      | 47     |
| 395    | 3   | 666   | 1271 | lgi 1204316      | lORFU [Lactococcus lactis]   | 1     | 67      | 47     |
| 415    | 1   | 1800  | 901  | lgi 882579       | lhypothetical protein (GB:U00014_4) [Haemophilus influenzae]                                 | 1     | 67      | 55     |
| 419    | 1   | 1799  | 903  | lgi 520752       | lICG Site No. 29739 [Escherichia coli]   | 1     | 67      | 46     |
| 474    | 1   | 2     | 796  | lgi 886906       | lputative [Bacillus subtilis]  | 1     | 67      | 48     |
| 485    | 2   | 1921  | 2226 | lgi 143434       | largininosuccinate synthetase [Streptomyces clavuligerus] pir S57659 S57659                  | 1     | 67      | 49     |
| 596    | 1   | 1728  | 865  | lgi 11303853     | largininosuccinate synthetase (EC 6.3.4.5) - treptomyces clavuligerus                        | 1     | 67      | 43     |
| 700    | 1   | 433   | 218  | lgi 1204628      | lRho Factor [Bacillus subtilis]  | 1     | 67      | 47     |
| 806    | 2   | 249   | 647  | lgi 677947       | lhypothetical protein (SP:P21498) [Haemophilus influenzae]                                   | 1     | 67      | 51     |
| 828    | 2   | 340   | 900  | lgi 1777761      | lAppC [Bacillus subtilis]  | 1     | 67      | 37     |
| 833    | 1   | 1407  | 916  | lgi 142996       | lIrrA [Synechococcus sp.]  | 1     | 67      | 41     |
| 856    | 1   | 1555  | 779  | lgi 1780224      | lregulatory protein [Bacillus subtilis]  | 1     | 67      | 38     |
| 888    | 1   | 1614  | 850  | lgi 437315       | l2K970.2 [Caenorhabditis elegans]  | 1     | 67      | 40     |
| 1034   | 1   | 1190  | 597  | lgi 1205113      | lTTG start codon [Bacillus licheniformis]  | 1     | 67      | 45     |
| 1062   | 1   | 636   | 319  | lgi 1303850      | lhypothetical protein (GB:L19201_15) [Haemophilus influenzae]                                | 1     | 67      | 41     |
| 1067   | 1   | 918   | 460  | lpir A32950 A329 | lprobable reductase protein - Leishmania major   | 1     | 67      | 54     |

| Contig | ORF | Start | Stop  | match     | match gene name | % sim  | % ident | length         |
|--------|-----|-------|-------|-----------|-----------------|--|---------|----------------|
| ID     | ID  | (nt)  | (nt)  | accession |                 |  |         | (nt)           |
| 1358   | 1   | 1     | 3     | 293       | gi 1001369      | hypothetical protein [Synechocystis sp.]                                   | 1       | 67   44   291  |
| 2181   | 1   | 1     | 3     | 302       | gi 1510416      | hypothetical protein (SP:SPJ466) [Methanococcus jannaschii]                | 1       | 67   48   300  |
| 3000   | 1   | 1     | 1     | 507       | gi 517205       | 67 kDa Myosin-crossreactive streptococcal antigen [Streptococcus yogenes]  | 1       | 67   56   507  |
| 3066   | 1   | 1     | 464   | 234       | gi 3088861      | GTG start codon [Lactococcus lactis]                                       | 1       | 67   46   231  |
| 3087   | 1   | 1     | 454   | 251       | gi 1205366      | oligopeptide transport ATP-binding protein [Haemophilus influenzae]        | 1       | 67   44   204  |
| 3101   | 1   | 1     | 2     | 256       | gi 1531541      | luproporphyrinogen III methyltransferase [Zea mays]                        | 1       | 67   55   255  |
| 3598   | 1   | 1     | 728   | 393       | gi 151259       | HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii] pir A44756 A44756  | 1       | 67   56   336  |
|        |     |       |       |           |                 | hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) Pseudomonas sp.          | 1       |                |
| 3765   | 1   | 2     | 584   | 366       | gi 557489       | lmend [Bacillus subtilis]  | 1       | 67   45   219  |
| 3788   | 1   | 1     | 658   | 398       | pir S52915 S529 | linitrate reductase alpha chain - Bacillus subtilis (fragment)             | 1       | 67   45   261  |
| 3883   | 1   | 1     | 2     | 265       | gi 1704397      | cystathionine beta-lyase [Arabidopsis thaliana]                            | 1       | 67   46   264  |
| 3926   | 1   | 1     | 2     | 340       | gi 1483199      | peptide-synthetase [Amycolatopsis mediterranei]                            | 1       | 67   44   339  |
| 4417   | 1   | 1     | 82    | 396       | gi 1205337      | ribonucleotide transport ATP-binding protein [Haemophilus influenzae]      | 1       | 67   46   315  |
| 2      | 1   | 3     | 3075  | 3989      | gi 535348       | CodV [Bacillus subtilis]   | 1       | 66   42   915  |
| 15     | 1   | 6     | 2273  | 2542      | gi 46491        | SmtB [Synechococcus PCC7942]   | 1       | 66   37   270  |
| 31     | 1   | 9     | 8059  | 7826      | gi 292046       | mucin [Homo sapiens]   | 1       | 66   44   234  |
| 31     | 1   | 10    | 9034  | 9258      | gi 1204545      | mercury scavenger protein [Haemophilus influenzae]                         | 1       | 66   48   225  |
| 32     | 1   | 6     | 6347  | 5253      | gi 998342       | inducible nitric oxide synthase [Gallus gallus]                            | 1       | 66   47   1095 |
| 44     | 1   | 13    | 8856  | 10124     | gi 1510751      | l-molybdenum cofactor biosynthesis moeA protein [Methanococcus jannaschii] | 1       | 66   46   1269 |
| 48     | 1   | 2     | 1276  | 2868      | gi 150209       | ORF 1 [Mycoplasma mycoides]  | 1       | 66   40   1593 |
| 58     | 1   | 8     | 7178  | 8428      | gi 665999       | hypothetical protein [Bacillus subtilis]                                   | 1       | 66   47   1251 |
| 62     | 1   | 7     | 5143  | 4370      | gi 1072398      | phaD gene product [Rhizobium meliloti]                                     | 1       | 66   40   774  |
| 70     | 1   | 14    | 11693 | 10998     | gi 809660       | deoxyribose phosphate aldolase [Bacillus subtilis] pir S49455 S49455       | 1       | 66   55   696  |
|        |     |       |       |           |                 | deoxyribose-phosphate aldolase (EC 4.1.2.4) - acillus subtilis             | 1       |                |
| 76     | 1   | 1     | 1     | 1305      | gi 142440       | ATP-dependent nuclelease [Bacillus subtilis]                               | 1       | 66   42   1305 |
| 91     | 1   | 6     | 9236  | 8205      | gi 704397       | cystathionine beta-lyase [Arabidopsis thaliana]                            | 1       | 66   43   1032 |
| 102    | 1   | 5     | 3810  | 3265      | gi 1204323      | hypothetical protein (SP:SP31805) [Haemophilus influenzae]                 | 1       | 66   41   546  |

## S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop   | match      | gene name   | % sim | % ident | length |
|--------|-----|--------|--------|------------|---|-------|---------|--------|
| ID     | ID  | (nt)   | (nt)   | accession  |   | (nt)  | (nt)    | (nt)   |
| 103    | 4   | 3418   | 2732   | gi 971344  | nitrate reductase gamma subunit [Bacillus subtilis] sp P42177 NARI_BACSU  | 66    | 48      | 687    |
|        |     |        |        |            | NITRATE REDUCTASE GAMMA CHAIN (EC 1.7.99.4). gi 1009369 Respiratory       |       |         |        |
|        |     |        |        |            | nitrate reductase [Bacillus subtilis] (SUB -160)                          |       |         |        |
| 109    | 6   | 4243   | 4674   | gi 170886  | glucosamine-6-phosphate deaminase [Candida albicans] pir A46652 A46652    | 66    | 45      | 432    |
|        |     |        |        |            | glucosamine-6-phosphate isomerase (EC 5.3.1.10) - east (Candida albicans) |       |         |        |
| 112    | 17  | 117491 | 117712 | gi 1323179 | ORF YGR11W [Saccharomyces cerevisiae]                                     | 66    | 33      | 222    |
| 116    | 2   | 4667   | 2637   | gi 1491813 | gamma-glutamyltranspeptidase [Bacillus subtilis]                          | 66    | 43      | 2031   |
| 150    | 5   | 3189   | 2989   | gi 1146224 | putative [Bacillus subtilis]  | 66    | 30      | 201    |
| 172    | 5   | 3264   | 3662   | gi 755152  | highly hydrophobic integral membrane protein [Bacillus subtilis]          | 66    | 41      | 399    |
|        |     |        |        |            | sp P42953 TAGG BACSU TEICHOIC ACID TRANSLOCATION PERMEASE PROTEIN AGG.    |       |         |        |
| 174    | 5   | 4592   | 3723   | gi 1146241 | lipoate synthetase [Bacillus subtilis]                                    | 66    | 49      | 870    |
| 175    | 4   | 3209   | 2880   | gi 642655  | lunkown [Rhizobium meliloti]  | 66    | 29      | 330    |
| 175    | 11  | 8743   | 7994   | gi 854655  | Na/H antiporter system [Bacillus alcalophilus]                            | 66    | 43      | 750    |
| 190    | 5   | 7079   | 5727   | gi 451072  | di-tripeptide transporter [Lactococcus lactis]                            | 66    | 40      | 1353   |
| 195    | 15  | 113919 | 113713 | gi 1322411 | lunkown [Mycobacterium tuberculosis]                                      | 66    | 42      | 207    |
| 217    | 3   | 2822   | 2595   | gi 1143542 | alternative stop codon [Rattus norvegicus]                                | 66    | 36      | 228    |
| 233    | 9   | 7133   | 6135   | gi 1458327 | F08F3.4 gene product [Caenorhabditis elegans]                             | 66    | 47      | 999    |
| 238    | 1   | 43     | 1041   | gi 809541  | Cbra protein [Erwinia chrysanthemi]                                       | 66    | 42      | 999    |
| 241    | 1   | 2102   | 1053   | gi 153067  | peptidoglycan hydrolase [Staphylococcus aureus]                           | 66    | 53      | 1050   |
| 261    | 1   | 1178   | 648    | gi 1510839 | M. jannaschii predicted coding region MJ0790 [Methanococcus jannaschii]   | 66    | 40      | 531    |
| 263    | 3   | 3731   | 2973   | gi 1205865 | tetrahydrodipicolinate N-succinyltransferase [Haemophilus influenzae]     | 66    | 47      | 759    |
| 272    | 8   | 6548   | 5484   | gi 882101  | high affinity nickel transporter [Alcaligenes eutrophus]                  | 66    | 44      | 1065   |
|        |     |        |        |            | sp P23516 H0XN_ALCEU HIGH-AFFINITY NICKEL TRANSPORT PROTEIN.              |       |         |        |
| 276    | 3   | 2805   | 2104   | gi 1208965 | hypothetical 23.3 kd protein [Escherichia coli]                           | 66    | 47      | 702    |
| 278    | 2   | 2830   | 1784   | gi 1488662 | phosphatase-associated protein [Bacillus subtilis]                        | 66    | 48      | 1047   |
| 278    | 3   | 3830   | 2952   | gi 303560  | ORF271 [Escherichia coli]   | 66    | 45      | 879    |
| 279    | 2   | 3894   | 2218   | gi 1185289 | 12-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Bacillus | 66    | 48      | 1677   |
|        |     |        |        |            | subtilis]   |       |         |        |
| 288    | 4   | 2535   | 2275   | gi 1256625 | putative [Bacillus subtilis]  | 66    | 42      | 261    |
| 292    | 2   | 1133   | 942    | gi 1511604 | M. jannaschii predicted coding region MJ1651 [Methanococcus jannaschii]   | 66    | 30      | 192    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop | match           | gene name  | % sim | % ident | length |
|--------|-----|-------|------|-----------------|--|-------|---------|--------|
| ID     | ID  | (nt)  | (nt) | accession       |  | (nt)  | (nt)    |        |
| 294    | 1   | 1116  | 1559 | gi 216314       | esterase [Bacillus stearothermophilus]                                     | 66    | 45      | 558    |
| 297    | 4   | 2913  | 1978 | gi 994794       | cytochrome a assembly facto [Bacillus subtilis] sp P24009 COXX_BACSU       | 66    | 45      | 936    |
|        |     |       |      |                 | PROBABLE CYTOCHROME C OXIDASE ASSEMBLY FACTOR.                             |       |         |        |
| 316    | 4   | 2053  | 2682 | gi 1107839      | alginic lyase [Pseudomonas aeruginosa]                                     | 66    | 40      | 630    |
| 338    | 4   | 2460  | 2302 | gi 520750       | biotin synthetase [Bacillus sphaericus]                                    | 66    | 58      | 159    |
| 339    | 1   | 1214  | 735  | gi 467468       | 17, 8-dihydro-6-hydroxymethyl-pterin-pyrophosphokinase [Bacillus subtilis] | 66    | 52      | 480    |
| 363    | 1   | 3     | 863  | gi 581649       | lepic gene product [Staphylococcus epidermidis]                            | 66    | 47      | 861    |
| 366    | 2   | 232   | 483  | gi 1103505      | unknown [Schizosaccharomyces pombe]  | 66    | 53      | 252    |
| 367    | 4   | 2468  | 1845 | sp P20692 TYRA_ | PREPHENATE DEHYDROGENASE (EC 1.3.1.12) (PDH).                              | 66    | 50      | 624    |
| 372    | 3   | 2150  | 1599 | gi 467416       | unknown [Bacillus subtilis]  | 66    | 38      | 552    |
| 378    | 1   | 212   | 1009 | gi 147309       | purine nucleoside phosphorylase [Escherichia coli]                         | 66    | 50      | 798    |
| 401    | 1   | 1     | 462  | gi 388263       | p-aminobenzoic acid synthase [Streptomyces griseus] pir JN0531 JM0531_P-   | 66    | 46      | 462    |
|        |     |       |      |                 | aminobenzoic acid synthase - Streptomyces griseus                          |       |         |        |
| 404    | 7   | 4826  | 5254 | gi 606744       | cytidine deaminase [Bacillus subtilis]                                     | 66    | 51      | 429    |
| 411    | 2   | 1738  | 1103 | gi 1460081      | unknown [Mycobacterium tuberculosis]                                       | 66    | 44      | 636    |
| 420    | 1   | 2     | 541  | gi 1046024      | Na <sup>+</sup> ATPase subunit J [Mycoplasma genitalium]                   | 66    | 49      | 540    |
| 431    | 1   | 1     | 858  | gi 1500008      | M. jannaschii predicted coding region MJ1154 [Methanococcus jannaschii]    | 66    | 50      | 858    |
| 443    | 7   | 5679  | 5299 | gi 852076       | MrGA [Bacillus subtilis]   | 66    | 46      | 381    |
| 444    | 3   | 3405  | 2413 | gi 153047       | lysostaphin (ttg start codon) [Staphylococcus simulans] pir A25881 A25881  | 66    | 51      | 993    |
|        |     |       |      |                 | lysostaphin precursor - Staphylococcus simulans sp P10547 LSTP_STASI       |       |         |        |
|        |     |       |      |                 | LYSOSTAPHIN PRECURSOR (EC 3.5.1.-)   |       |         |        |
| 561    | 1   | 956   | 480  | gi 1204905      | lDNA-3-methyladenine glycosidase I [Haemophilus influenzae]                | 66    | 45      | 477    |
| 562    | 3   | 1066  | 1383 | gi 1046082      | M. genitalium predicted coding region MG372 [Mycoplasma genitalium]        | 66    | 52      | 318    |
| 576    | 1   | 11    | 724  | gi 305014       | lORF_0234 [Escherichia coli]   | 66    | 43      | 714    |
| 577    | 3   | 1190  | 903  | gi 1001353      | hypothetical protein [Synechocystis sp.]                                   | 66    | 52      | 288    |
| 584    | 1   | 2     | 331  | sp P24204 YEBA_ | HYPOTHETICAL 46.7 KD PROTEIN IN MSBB-RUVB INTERGENIC REGION (ORFU).        | 66    | 48      | 330    |
| 592    | 1   | 1410  | 706  | gi 928839       | lORF266; putative [Lactococcus lactis phage BK5-T]                         | 66    | 51      | 705    |
| 601    | 1   | 1433  | 720  | gi 1488695      | novel antigen; orf-2 [Staphylococcus aureus]                               | 66    | 55      | 714    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop | match        | match gene name   |
|--------|-----|-------|------|--------------|---|
| ID     | ID  | (nt)  | (nt) | accession    |   |
| 619    | 3   | 468   | 845  | lgi 746573   | similar to M. musculus transport system membrane protein, N ramp PIR:A40739 |
|        |     |       |      |              | and S. cerevisiae SMF1 protein (PIR:A45154) Caenorhabditis elegans          |
| 706    | 2   | 561   | 355  | lgi 804808   | unknown protein [Rattus norvegicus]   |
| 734    | 2   | 673   | 512  | lgi 1519085  | phosphatidylcholine binding immunoglobulin heavy chain IgM variable region  |
|        |     |       |      |              | [Mus musculus]  |
| 740    | 1   | 3     | 317  | lgi 11209272 | argininosuccinate lyase [Campylobacter jejuni]                              |
|        |     |       |      |              | alkaline phosphatase-like protein [Lactococcus lactis] pir S39339 S39339    |
| 764    | 1   | 310   | 747  | lgi 435296   | alkaline phosphatase-like protein - Lactococcus actis                       |
|        |     |       |      |              |   |
| 852    | 1   | 338   | 171  | lgi 536955   | ICG Site No. 361 [Escherichia coli]   |
|        |     |       |      |              |   |
| 886    | 1   | 3     | 158  | lgi 289272   | ferrichrome-binding protein [Bacillus subtilis]                             |
|        |     |       |      |              |   |
| 889    | 1   | 462   | 232  | lgi 833061   | lHCMVUL77 (AA 1-642) [Human cytomegalovirus]                                |
|        |     |       |      |              |   |
| 893    | 1   | 2     | 247  | lgi 149008   | putative [Helicobacter pylori]  |
|        |     |       |      |              |   |
| 900    | 1   | 1425  | 733  | lgi 580842   | lF3 [Bacillus subtilis]   |
|        |     |       |      |              |   |
| 906    | 2   | 2300  | 1473 | lgi 1790945  | laryl-alcohol dehydrogenase [Bacillus subtilis]                             |
|        |     |       |      |              |   |
| 947    | 1   | 79    | 549  | lgi 410117   | lDiaminopimelate decarboxylase [Bacillus subtilis]                          |
|        |     |       |      |              |   |
| 950    | 1   | 1100  | 552  | lgi 48713    | lorf145 [Staphylococcus aureus]   |
|        |     |       |      |              |   |
| 955    | 2   | 89    | 475  | lgi 1204390  | luridine kinase (uridine monophosphokinase) [Haemophilus influenzae]        |
|        |     |       |      |              |   |
| 981    | 2   | 1308  | 997  | lgi 457146   | lrhoptry protein [Plasmidium yoelii]  |
|        |     |       |      |              |   |
| 986    | 1   | 25    | 315  | lgi 305002   | lORF f356 [Escherichia coli]  |
|        |     |       |      |              |   |
| 1057   | 1   | 3     | 203  | lgi 1303853  | lYggF [Bacillus subtilis]   |
|        |     |       |      |              |   |
| 1087   | 1   | 1     | 294  | lgi 575913   | lunknown [Saccharomyces cerevisiae]   |
|        |     |       |      |              |   |
| 1105   | 1   | 1     | 231  | lgi 1045799  | lmethylgalactoside permease ATP-binding protein [Mycoplasma genitalium]     |
|        |     |       |      |              |   |
| 1128   | 1   | 2     | 574  | lgi 1001493  | lhypothetical protein [Synechocystis sp.]                                   |
|        |     |       |      |              |   |
| 1150   | 1   | 498   | 250  | lgi 1499034  | lM. jannaschii predicted coding region MJ0255 [Methanococcus jannaschii]    |
|        |     |       |      |              |   |
| 1180   | 2   | 707   | 453  | lgi 215908   | lDNA polymerase (g43) [Bacteriophage T4]                                    |
|        |     |       |      |              |   |
| 1208   | 1   | 1123  | 587  | lgi 1256653  | lDNA-binding protein [Bacillus subtilis]                                    |
|        |     |       |      |              |   |
| 1342   | 1   | 1     | 402  | lgi 1208474  | lhypothetical protein [Synechocystis sp.]                                   |
|        |     |       |      |              |   |
| 1761   | 2   | 589   | 398  | lgi 215811   | ltail fiber protein [Bacteriophage T3]                                      |
|        |     |       |      |              |   |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF  | Start | Stop | match     | gene name | % sim           | % ident   | length |
|--------|------|-------|------|-----------|-----------|-----------------|---|--------|
| ID     | ID   | (nt)  | (nt) | accession |           | (nt)            | (nt)  |        |
| 1      | 1983 | 1     | 499  | 1         | 251       | gi 1045935      | lDNA helicase 1I [Mycoplasma genitalium]                                    | 66     |
| 1      | 2103 | 2     | 176  | 1         | 400       | gi 929798       | precursor for the major merozoite surface antigens [Plasmodium aliciparum]  | 66     |
| 1      | 2341 | 1     | 373  | 1         | 188       | gi 1256623      | lexodeoxyribonuclease [Bacillus subtilis]                                   | 66     |
| 1      | 2458 | 1     | 325  | 1         | 164       | gi 1019410      | Unknown [Schizosaccharomyces pombe]   | 66     |
| 1      | 2505 | 1     | 468  | 1         | 235       | gi 1510394      | putative transcriptional regulator [Methanococcus jannaschii]               | 66     |
| 1      | 2525 | 1     | 558  | 1         | 280       | gi 1000695      | cytotoxin L [Clostridium sordellii]   | 66     |
| 1      | 2935 | 1     | 3    | 1         | 275       | gi 765073       | autolysin [Staphylococcus aureus]   | 66     |
| 1      | 3005 | 1     | 114  | 1         | 305       | gi 1205784      | heterocyst maturation protein [Haemophilus influenzae]                      | 66     |
| 1      | 3048 | 1     | 80   | 1         | 277       | gi 1303813      | YqEW [Bacillus subtilis]  | 66     |
| 1      | 3071 | 1     | 1    | 1         | 189       | gi 1070014      | protein-dependent [Bacillus subtilis]                                       | 66     |
| 1      | 3081 | 1     | 404  | 1         | 225       | gi 984212       | Unknown [Schizosaccharomyces pombe]   | 66     |
| 1      | 3090 | 2     | 580  | 1         | 386       | gi 1204987      | DNA polymerase III, alpha chain [Haemophilus influenzae]                    | 66     |
| 1      | 3318 | 1     | 1    | 1         | 387       | gi 1009366      | Respiratory nitrate reductase [Bacillus subtilis]                           | 66     |
| 1      | 3739 | 1     | 798  | 1         | 400       | gi 1109684      | lProv [Bacillus subtilis]   | 66     |
| 1      | 3796 | 1     | 402  | 1         | 202       | gi 853760       | acyl-CoA dehydrogenase [Bacillus subtilis]                                  | 66     |
| 1      | 3924 | 1     | 595  | 1         | 347       | gi 563952       | gluconate permease [Bacillus licheniformis]                                 | 66     |
| 1      | 4240 | 1     | 3    | 1         | 350       | gi 151259       | HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii] piraA44756 A44756   | 66     |
| 1      | 4604 | 1     | 7    | 1         | 234       | pir A26713 BHHC | hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) Pseudomonas sp.           | 66     |
| 1      | 4    | 9     | 8846 | 1         | 9750      | gi 145646       | hemocyanin subunit II - Atlantic horseshoe crab                             | 66     |
| 1      | 6    | 5     | 2708 | 1         | 3565      | gi 887824       | cynR [Escherichia coli]   | 65     |
| 1      | 13   | 1     | 1993 | 1         | 998       | gi 143402       | ORF_0310 [Escherichia coli]   | 65     |
| 1      | 15   | 7     | 2493 | 1         | 3524      | gi 1403126      | recombination protein (ttg start codon) [Bacillus subtilis] gi 1303923 RecN | 65     |
| 1      | 18   | 3     | 1908 | 1         | 1372      | gi 349187       | [Bacillus subtilis]   | 65     |
| 1      | 21   | 3     | 1467 | 1         | 2492      | gi 149518       | czCD gene product [Alcaligenes eutrophus]                                   | 65     |
| 1      | 25   | 4     | 3374 | 1         | 4312      | gi 1502420      | phosphoribosyl anthranilate transferase [Lactococcus lactis] -              | 65     |
|        |      |       |      |           |           |                 | pir S35126 S35126 anthranilate phosphoribosyltransferase (EC 4.2.18) -      | 65     |
|        |      |       |      |           |           |                 | Lactococcus lactis subsp. lactis  | 65     |
|        |      |       |      |           |           |                 | malonyl-CoA:Acyl carrier protein transacylase [Bacillus subtilis]           | 44     |
|        |      |       |      |           |           |                 |   | 939    |

*S. aureus* - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop   | match      | gene name  | % sim  | % ident | length |      |
|--------|-----|--------|--------|------------|--|--|---------|--------|------|
| ID     | ID  | (nt)   | (nt)   | accession  |  | (nt)   | (nt)    |        |      |
| 27     | 1   | 2      | 390    | 626        | gi 1212729   | YqhJ [Bacillus subtilis]   | 65      | 45     | 237  |
| 31     | 112 | 11040  | 10387  | 1gi 509245 | D-hydroxyisocaproate dehydrogenase [Lactobacillus delbrueckii] | 65   | 41      | 654    |      |
| 38     | 124 | 119172 | 19528  | 1gi 547519 | lH-protein [Flavervia crongquistii]                            | 65   | 41      | 357    |      |
| 44     | 1   | 2      | 790    | 1746       | 1gi 4058882  | lyeIK [Escherichia coli]   | 65      | 46     | 957  |
| 44     | 112 | 1      | 9356   | 8832       | 1gi 1205905  | Imolybdenum cofactor biosynthesis protein [Haemophilus influenzae]                   | 65      | 50     | 525  |
| 45     | 1   | 8      | 6635   | 7588       | 1gi 493074   | 1ApbA protein [Salmonella typhimurium]   | 65      | 46     | 954  |
| 51     | 1   | 2      | 580    | 1503       | 1gi 580897   | OppB gene product [Bacillus subtilis]  | 65      | 45     | 924  |
| 52     | 1   | 1      | 225    | 953        | 1gi 1205518  | INAD(PtH-Flavin oxidoreductase [Haemophilus influenzae]                              | 65      | 45     | 729  |
| 55     | 1   | 4      | 1339   | 1058       | 1pir A44159 A444   | 1trponin T beta TnT-5 - rabbit   | 65      | 41     | 282  |
| 67     | 1   | 9      | 17421  | 8272       | 1gi 143607   | 1sporulation protein [Bacillus subtilis]   | 65      | 42     | 852  |
| 73     | 1   | 5      | 4446   | 5375       | 1gi 1204896  | 1lysophospholipase L2 [Haemophilus influenzae]                                       | 65      | 37     | 930  |
| 74     | 1   | 1      | 954    | 1478       | 1gi 1204844  | 1H. influenzae predicted coding region HI0594 [Haemophilus influenzae]               | 65      | 50     | 477  |
| 77     | 1   | 1      | 2      | 1757       | 1gi 1046082  | 1M. genitalium predicted coding region MG372 [Mycoplasma genitalium]                 | 65      | 46     | 756  |
| 77     | 1   | 2      | 1795   | 1433       | 1gi 1222116  | 1permease [Haemophilus influenzae]   | 65      | 37     | 639  |
| 81     | 1   | 3      | 4728   | 3454       | 1gi 1001708  | 1hypothetical protein [Synechocystis sp.]  | 65      | 49     | 1275 |
| 91     | 1   | 7      | 8548   | 8357       | 1gi 1399263  | 1cystathionine beta-lyase [Emericella nidulans]                                      | 65      | 40     | 192  |
| 98     | 1   | 3      | 1608   | 1988       | 1gi 467423   | 1unknown [Bacillus subtilis]   | 65      | 38     | 381  |
| 98     | 1   | 4      | 12250  | 12987      | 1gi 467424   | 1unknown [Bacillus subtilis]   | 65      | 45     | 738  |
| 102    | 1   | 3      | 2598   | 2119       | 1gi 1511532  | 1N-terminal acetyltransferase complex, subunit ARD1 [Methanococcus jannaschii]       | 65      | 39     | 480  |
| 102    | 1   | 4      | 3647   | 2862       | 1gi 1204637  | 1H. influenzae predicted coding region HI0388 [Haemophilus influenzae]               | 65      | 32     | 786  |
| 103    | 1   | 9      | 10851  | 9841       | 1gi 142695   | 1S-adenosyl-L-methionine:uroporphyrinogen III methyltransferase Bacillus megaterium] | 65      | 47     | 1011 |
| 103    | 1   | 10     | 110439 | 10119      | 1gi 710021   | 1nitrite reductase (nirD) [Bacillus subtilis]  | 65      | 51     | 321  |
| 106    | 1   | 2      | 262    | 1140       | 1gi 39881  | 1ORF 311 (AA 1-311) [Bacillus subtilis]  | 65      | 44     | 879  |
| 109    | 1   | 5      | 3909   | 4268       | 1gi 1204399  | 1glucosamine-6-phosphate deaminase protein [Haemophilus influenzae]                  | 65      | 44     | 360  |
| 109    | 1   | 10     | 7165   | 8595       | 1gi 536955   | 1CG Site No. 361 [Escherichia coli]  | 65      | 41     | 1431 |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop   | match       | match gene name  | % sim | % ident | length |
|--------|-----|--------|--------|-------------|--|-------|---------|--------|
| ID     | ID  | (nt)   | (nt)   | accession   |  | (nt)  | (nt)    | (nt)   |
| 110    | 4   | 3688   | 3915   | gi 407881   | stringent response-like protein [Streptococcus equisimilis]<br>  pir S39975 S39975 stringent response-like protein - Streptococcus<br>  quissimilis                                      | 65    | 45      | 228    |
| 110    | 5   | 3882   | 4295   | gi 407880   | ORF1 [Streptococcus equisimilis]   | 65    | 50      | 414    |
| 110    | 6   | 4231   | 4380   | gi 1139574  | Orf2 [Streptomyces griseus]  | 65    | 56      | 150    |
| 112    | 10  | 9218   | 8640   | gi 1204571  | [H. influenzae predicted coding region HI0318 [Haemophilus influenzae]   | 65    | 52      | 579    |
| 112    | 12  | 112049 | 111288 | gi 710496   | transcriptional activator protein [Bacillus brevis]  | 65    | 32      | 762    |
| 125    | 1   | 1      | 2      | gi 1151158  | repeat organellar protein [Plasmodium chabaudi]  | 65    | 39      | 201    |
| 126    | 1   | 3      | 422    | gi 37589    | precursor [Homo sapiens]   | 65    | 46      | 420    |
| 127    | 11  | 110733 | 112658 | gi 1064809  | homologous to sp:HTRA_ECOLI [Bacillus subtilis]  | 65    | 41      | 1926   |
| 143    | 8   | 7543   | 7004   | gi 216513   | lmutator mutT (AT-GC transversion) [Escherichia coli]  | 65    | 56      | 540    |
| 145    | 5   | 3587   | 3838   | gi 1209768  | D02_orf569 [Mycoplasma pneumoniae]   | 65    | 27      | 252    |
| 150    | 4   | 3482   | 2841   | gi 1146225  | putative [Bacillus subtilis]   | 65    | 37      | 642    |
| 166    | 1   | 3858   | 1948   | gi 148304   | lbeta-1,4-N-acetylmuramoylhydrolase [Enterococcus hirae] pir A42296 A42296   | 65    | 50      | 1911   |
|        |     |        |        |             | lysozyme 2 (EC 3.2.1.-) precursor - Enterococcus hirae (ATCC 9790)   |       |         |        |
| 188    | 6   | 3195   | 4178   | gi 151943   | lORF3; putative [Rhodobacter capsulatus]   | 65    | 46      | 984    |
| 189    | 9   | 4982   | 4785   | gi 58812    | lORF IV (AA 1-489) [Figwort mosaic virus]  | 65    | 40      | 198    |
| 195    | 6   | 17908  | 15272  | gi 145220   | lalanyl-tRNA synthetase [Escherichia coli]   | 65    | 49      | 2637   |
| 195    | 7   | 110599 | 8104   | gi 882711   | lexonuclease V alpha-subunit [Escherichia coli]  | 65    | 38      | 2496   |
| 206    | 116 | 116896 | 118191 | gi 408115   | lornithine acetyltransferase [Bacillus subtilis]   | 65    | 53      | 1296   |
| 217    | 4   | 3844   | 3215   | gi 1205974  | l5'guanylate kinase [Haemophilus influenzae]   | 65    | 41      | 630    |
| 220    | 4   | 5265   | 3751   | gi 580920   | lrodD (graA) polypeptide (AA 1-673) [Bacillus subtilis] pir S06048 S06048  | 65    | 40      | 1515   |
|        |     |        |        |             | probable rodD protein - Bacillus subtilis sp P13484 TAGE BACSU PROBABLE<br>  POLY(GLYCEROL-PHOSPHATE) LPHA-GLUCOSYLTRANSFERASE (EC 2.4.1.52) (TECHOIC<br>  ACID BIOSYNTHESIS PROTEIN E). |       |         |        |
| 236    | 5   | 2327   | 3709   | gi 11146200 | lDNA or RNA helicase, DNA-dependent ATPase [Bacillus subtilis]   | 65    | 46      | 1383   |
| 237    | 3   | 1902   | 2513   | gi 149379   | lHisBd [Lactococcus lactis]  | 65    | 46      | 612    |
| 241    | 4   | 4968   | 4195   | gi 1205308  | lribonuclease HII (EC 31264) (RNASE HII) [Haemophilus influenzae]  | 65    | 50      | 774    |
| 252    | 1   | 1278   | 940    | gi 1204989  | lhypothetical protein (GB:U00022_9) [Haemophilus influenzae]   | 65    | 40      | 339    |
| 261    | 5   | 4780   | 3794   | gi 145927   | lfecD [Escherichia coli]   | 65    | 43      | 987    |

## S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF ID | Start (nt) | Stop (nt) | match accession | match gene name   | % sim | % ident | length (nt) |
|--------|--------|------------|-----------|-----------------|---|-------|---------|-------------|
| 1      | 274    | 1          | 3         | 278             | gi 496558  orfX [Bacillus subtilis]   | 1     | 65      | 42          |
| 1      | 301    | 2          | 982       | 815             | gi 467418  unknown [Bacillus subtilis]  | 1     | 65      | 45          |
| 1      | 307    | 4          | 3586      | 2864            | gi 1070014  protein-dependent [Bacillus subtilis]   | 1     | 65      | 40          |
| 1      | 335    | 2          | 2286      | 1399            | gi 146913  N-acetylglucosamine transport protein [Escherichia coli] pirB29895 WQEC2N  | 1     | 65      | 50          |
|        |        |            |           |                 | phosphotransferase system enzyme II (EC 7.1.69), N-acetylglucosamine-specific - Escherichia coli sp P09323 PTAA_ECOLI PTS SYSTEM, N-ACETYLGLUCOSAMINE-SPECIFIC IIABC COMPONENT (EIIA) |       |         | 888         |
| 1      | 338    | 5          | 4120      | 3170            | gi 1277029  biotin synthase [Bacillus subtilis]   | 1     | 65      | 49          |
| 1      | 343    | 3          | 1490      | 2800            | gi 143264  membrane-associated protein [Bacillus subtilis]  | 1     | 65      | 48          |
| 1      | 344    | 4          | 2761      | 2531            | gi 1050540  tRNA-glutamine synthetase [Lupinus luteus]  | 1     | 65      | 34          |
| 1      | 358    | 3          | 3421      | 3621            | gi 1146220  NAD+ dependent glycerol-3-phosphate dehydrogenase [Bacillus subtilis]   | 1     | 65      | 47          |
| 1      | 364    | 1          | 238       | 699             | gi 1340128  ORF1 [Staphylococcus aureus]  | 1     | 65      | 51          |
| 1      | 379    | 1          | 1         | 576             | gi 143331  alkaline phosphatase regulatory protein [Bacillus subtilis]  | 1     | 65      | 40          |
|        |        |            |           |                 | pirA27650 A27650 regulatory protein phoR - Bacillus subtilis sp P23535 PHOR_BACSU ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN HOR (EC 2.7.3.-).                                     |       |         | 576         |
| 1      | 379    | 3          | 3666      | 4346            | gi 143268  dihydrolipoamide transsuccinylase (ochB; EC 2.3.1.61) [Bacillus subtilis]  | 1     | 65      | 50          |
| 1      | 428    | 1          | 187       | 483             | gi 1420165  ORF YOR195w [Saccharomyces cerevisiae]  | 1     | 65      | 45          |
| 1      | 438    | 2          | 272       | 838             | gi 143498  degS protein [Bacillus subtilis]   | 1     | 65      | 38          |
| 1      | 444    | 11         | 9280      | 10215           | gi 1204756  ribokinase [Haemophilus influenzae]   | 1     | 65      | 47          |
| 1      | 449    | 2          | 1241      | 1531            | gi 599848  Na/H antiporter homolog [Lactococcus lactis]   | 1     | 65      | 41          |
| 1      | 478    | 2          | 1452      | 865             | gi 1045942  glycyl-tRNA synthetase [Mycoplasma genitalium]  | 1     | 65      | 39          |
| 1      | 479    | 1          | 1032      | 517             | gi 1498192  putative [Pseudomonas aeruginosa]   | 1     | 65      | 40          |
| 1      | 480    | 6          | 4312      | 5637            | gi 415662  UDP-N-acetylglucosamine 1-carboxyvinyl transferase [Acinetobacter alcoaceticus]  | 1     | 65      | 48          |
|        |        |            |           |                 |   |       |         | 1326        |
| 1      | 484    | 1          | 2         | 430             | gi 146551  transmembrane protein (kdpD) [Escherichia coli]  | 1     | 65      | 44          |
| 1      | 499    | 1          | 54        | 932             | gi 603456  reductase [Leishmania major]   | 1     | 65      | 53          |
| 1      | 505    | 1          | 914       | 459             | gi 1518853  OafA [Salmonella typhimurium]   | 1     | 65      | 39          |
|        |        |            |           |                 |   |       |         | 456         |
| 1      | 571    | 2          | 1509      | 883             | gi 49399  open reading frame upstream glnE [Escherichia coli] ir S37754 S37754  | 1     | 65      | 44          |
|        |        |            |           |                 | hypothetical protein XE (glnE 5' region) - cherichia coli   |       |         | 627         |
| 1      | 611    | 2          | 506       | 270             | gi 10961  RAP-2 [Plasmodium falciparum]   | 1     | 65      | 40          |
|        |        |            |           |                 |   |       |         | 237         |

| Contig | ORF | Start  | Stop  | match           | gene name   | % sim | % ident | length |
|--------|-----|--------|-------|-----------------|---|-------|---------|--------|
| ID     | ID  | (nt)   | (nt)  | accession       |   | (nt)  | (nt)    |        |
| 705    | 1   | 564    | 1 283 | gi 710020       | Initrite reductase (nirB) [Bacillus subtilis]   | 65    | 52      | 282    |
| 712    | 1 1 | 1 177  | 1 177 | gi 289272       | ferrichrome-binding protein [Bacillus subtilis]   | 65    | 37      | 177    |
| 712    | 2   | 1 196  | 1 354 | gi 289272       | ferrichrome-binding protein [Bacillus subtilis]   | 65    | 37      | 159    |
| 743    | 1 1 | 2 631  | 1 631 | gi 310631       | ATP binding protein [Streptococcus gordonii]  | 65    | 45      | 630    |
| 749    | 2   | 1 393  | 1 779 | gi 467374       | single strand DNA binding protein [Bacillus subtilis]   | 65    | 29      | 387    |
| 762    | 1   | 1 1698 | 1 850 | gi 160399       | multidrug resistance protein [Plasmodium falciparum]  | 65    | 48      | 849    |
| 788    | 1   | 1 85   | 1 315 | gi 1129096      | unknown protein [Bacillus sp.]  | 65    | 35      | 231    |
| 850    | 1 1 | 1 408  | 1 408 | gi 1006604      | hypothetical protein [Synechocystis sp.]  | 65    | 37      | 408    |
| 908    | 1 1 | 1 444  | 1 444 | gi 1199546      | 12362 [Saccharomyces cerevisiae]  | 65    | 46      | 444    |
| 925    | 1 1 | 1 174  | 1 174 | gi 1256653      | DNA-binding protein [Bacillus subtilis]   | 65    | 54      | 174    |
| 1031   | 1   | 1 26   | 1 232 | gi 238657       | AppC:cytochrome d oxidase, subunit I homolog [Escherichia coli, K12, <i>epitope, 514 aa</i> ]   | 65    | 47      | 207    |
| 1037   | 1 1 | 1 414  | 1 262 | gi 1491813      | gamma-glutamyltranspeptidase [Bacillus subtilis]  | 65    | 46      | 153    |
| 1053   | 1 1 | 1 348  | 1 175 | gi 642655       | unknown [Rhizobium meliloti]  | 65    | 34      | 174    |
| 1149   | 1 1 | 1 1399 | 1 752 | gi 1162980      | ribulose-5-phosphate 3-epimerase [Spinacia oleracea]  | 65    | 48      | 648    |
| 1214   | 1 1 | 1 881  | 1 495 | gi 1255959      | lactam utilization protein [Haemophilus influenzae]   | 65    | 45      | 387    |
| 1276   | 1 1 | 1 476  | 1 276 | pir S35493 S354 | site-specific DNA-methyltransferase StsI (EC 2.1.1.-) - Streptococcus <i>sanguis</i>  | 65    | 35      | 201    |
| 1276   | 1 2 | 1 900  | 1 577 | gi 473794       | 'ORF' [Escherichia coli]  | 65    | 34      | 324    |
| 2057   | 1   | 1 272  | 1 138 | gi 633699       | Trsh [Yersinia enterocolitica]  | 65    | 21      | 135    |
| 2521   | 1 1 | 1 336  | 1 169 | gi 11045789     | hypothetical protein (GB:U14003_76) [Mycoplasma genitalium]   | 65    | 41      | 168    |
| 2974   | 1   | 1 590  | 1 297 | gi 152052       | lenantionerase-selective amidase [Rhodococcus sp.]  | 65    | 45      | 294    |
| 3031   | 1   | 1 306  | 1 154 | pir JQ1024 JQ10 | hypothetical 30k protein (DmRP140 5' region) - fruit fly (Drosophila <i>melanogaster</i> )  | 65    | 45      | 153    |
| 3069   | 1   | 3      | 1 278 | gi 14906        | product homologous to E.coli thioredoxin reductase: J.Biol.Chem. 1988)  | 65    | 46      | 276    |
|        |     |        |       |                 | 263:9015-9019, and to F52a protein of alkyl hydroperoxide eductase from <i>S.typhimurium</i> : J.Biol.Chem. (1990) 265:10535-10540; pen reading frame A |       |         |        |
|        |     |        |       |                 | [Clostridium pasteurianum]  |       |         |        |
| 3146   | 1   | 1 282  | 1 142 | gi 49315        | ORF1 gene product [Bacillus subtilis]   | 65    | 47      | 141    |
| 3170   | 1   | 1 679  | 1 341 | gi 1507711      | indolepyruvate decarboxylase [Erwinia herbicola]  | 65    | 44      | 339    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop   | match       | match gene name   | % sim | % ident | length |
|--------|-----|--------|--------|-------------|---|-------|---------|--------|
| ID     | ID  | (nt)   | (nt)   | accession   |   | (nt)  | (nt)    | (nt)   |
| 3546   | 1   | 1      | 303    | lgi 450688  | hsdM gene of Ecoprr1 gene product [Escherichia coli] pir S38437 S38437 hsdM | 65    | 42      | 303    |
|        |     |        |        |             | protein - Escherichia coli pir S09629 S09629 hypothetical protein A -       |       |         |        |
|        |     |        |        |             | Escherichia coli (SUB 40-520)   |       |         |        |
| 3782   | 1   | 2      | 328    | lgi 166412  | NADH-glutamate synthase [Medicago sativa]                                   | 65    | 42      | 327    |
| 3990   | 1   | 374    | 189    | lgi 1009366 | Respiratory nitrate reductase [Bacillus subtilis]                           | 65    | 53      | 186    |
| 4032   | 1   | 613    | 308    | lgi 1323127 | lORF YGR087C [Saccharomyces cerevisiae]                                     | 65    | 50      | 306    |
| 4278   | 2   | 726    | 364    | lgi 1197667 | vitellogenin [Anolis pulchellus]  | 65    | 42      | 363    |
| 19     | 4   | 4259   | 5518   | lgi 145727  | ldeaD [Escherichia coli]  | 64    | 45      | 1260   |
| 19     | 6   | 7639   | 6926   | lgi 1016232 | lycf27 gene product [Cyanophora paradoxa]                                   | 64    | 36      | 714    |
| 20     | 8   | 7053   | 6454   | lgi 765073  | lautolysin [Staphylococcus aureus]  | 64    | 47      | 600    |
| 31     | 13  | 112706 | 11537  | lgi 414009  | lipa-85d gene product [Bacillus subtilis]                                   | 64    | 45      | 1170   |
| 33     | 4   | 2388   | 4364   | lgi 1204696 | lfructose-permease IIBC component [Haemophilus influenzae]                  | 64    | 47      | 1977   |
| 36     | 3   | 1871   | 3013   | lgi 290503  | lglutamate permease [Escherichia coli]                                      | 64    | 40      | 1143   |
| 37     | 6   | 4065   | 4409   | lgi 39815   | lorf 2 gene product [Bacillus subtilis]                                     | 64    | 46      | 345    |
| 45     | 9   | 17852  | 18760  | lgi 1230585 | lnucleotide sugar epimerase [Vibrio cholerae 0139]                          | 64    | 53      | 909    |
| 53     | 3   | 1540   | 1899   | lgi 1303961 | lYqjJ [Bacillus subtilis]   | 64    | 50      | 360    |
| 56     | 6   | 4793   | 3855   | lgi 457514  | lglTC [Bacillus subtilis]   | 64    | 45      | 939    |
| 56     | 124 | 130002 | 130247 | lgi 470331  | lsimilar to zinc fingers [Caenorhabditis elegans]                           | 64    | 42      | 246    |
| 62     | 4   | 2759   | 2421   | lgi 642655  | lunknown [Rhizobium meliloti]   | 64    | 28      | 339    |
| 85     | 6   | 7178   | 6027   | lgi 457702  | l5-aminoimidazole ribonucleotide-carboxilase [Pichia methanolica]           | 64    | 46      | 1152   |
|        |     |        |        |             | pir S39112 S39112 phosphoribosylaminoimidazole carboxylase (EC .1.1.21) -   |       |         |        |
|        |     |        |        |             | yeast (Pichia methanolica)  |       |         |        |
| 96     | 9   | 9251   | 10030  | lgi 1511513 | lABC transporter, probable ATP-binding subunit [Methanococcus jannaschii]   | 64    | 42      | 780    |
| 100    | 1   | 1      | 600    | lgi 765073  | lautolysin [Staphylococcus aureus]  | 64    | 44      | 600    |
| 106    | 5   | 3868   | 4854   | lgi 466778  | llysine specific permease [Escherichia coli]                                | 64    | 46      | 987    |
| 123    | 2   | 838    | 554    | lgi 467484  | lunknown [Bacillus subtilis]  | 64    | 47      | 285    |
| 127    | 8   | 7514   | 7810   | lgi 210061  | lserotype-specific antigen [African horse sickness virus] pir S27891 S27891 | 64    | 28      | 297    |
|        |     |        |        |             | capsid protein VP2 - African horse sickness virus                           |       |         |        |
| 131    | 7   | 7134   | 6721   | lgi 1511160 | lM. jannaschii predicted coding region M11163 [Methanococcus jannaschii]    | 64    | 46      | 414    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop   | match     | match gene name | % sim   | % ident                   | length |      |     |
|--------|-----|-------|--------|-----------|-----------------|---|---------------------------|--------|------|-----|
| ID     | ID  | (nt)  | (nt)   | accession |                 |   |                           | (nt)   |      |     |
| 1      | 142 | 5     | 5455   | 4817      | gi 1173517      | Riboflavin synthase alpha subunit [Actinobacillus pleuropneumoniae]           | 64                        | 44     | 639  |     |
| 1      | 143 | 1     | 709    | 356       | pir A32950 A329 | probable reductase protein - Leishmania major                                 | 64                        | 52     | 354  |     |
| 1      | 149 | 10    | 3555   | 3295      | gi 398151       | Major surface antigen MSG2 [Pneumocystis carinii]                             | 64                        | 44     | 261  |     |
| 1      | 154 | 4     | 3134   | 2307      | gi 984587       | DinP [Escherichia coli]   | 64                        | 50     | 828  |     |
| 1      | 161 | 5     | 3855   | 4880      | gi 903304       | lORF72 [Bacillus subtilis]  | 64                        | 37     | 1026 |     |
| 1      | 165 | 1     | 33     | 791       | gi 467483       | lunknow [Bacillus subtilis]   | 64                        | 38     | 759  |     |
| 1      | 175 | 6     | 6355   | 4844      | gi 1072398      | lphaD gene product [Rhizobium meliloti]                                       | 64                        | 42     | 1512 |     |
| 1      | 188 | 3     | 2042   | 2500      | gi 1001961      | MHC class II analog [Staphylococcus aureus]                                   | 64                        | 45     | 459  |     |
| 1      | 195 | 14    | 113667 | 13446     | gi 396380       | lNo definition line found [Escherichia coli]                                  | 64                        | 47     | 222  |     |
| 1      | 206 | 15    | 116429 | 116938    | gi 304134       | larcC [Bacillus stearothermophilus]   | 64                        | 49     | 510  |     |
| 1      | 215 | 1     | 560    | 282       | gi 142359       | lORF 6 [Azotobacter vinelandii]   | 64                        | 39     | 279  |     |
| 1      | 243 | 7     | 7818   | 6928      | gi 414014       | lipa-90d gene product [Bacillus subtilis]                                     | 64                        | 49     | 891  |     |
| 1      | 258 | 2     | 1330   | 845       | gi 664754       | lP17 [Listeria monocytogenes]   | 64                        | 38     | 486  |     |
| 1      | 259 | 1     | 462    | 232       | gi 1499663      | lM. jannaschii predicted coding region MJ0837 [Methanococcus jannaschii]      | 64                        | 52     | 231  |     |
| 1      | 263 | 6     | 6565   | 5567      | gi 142828       | laspartate semialdehyde dehydrogenase [Bacillus subtilis]                     | 64                        | 48     | 999  |     |
| 1      |     |       |        |           |                 | lsp Q0479 lDHAS_BACSU ASPARTATE-SEMALDEHYDE DEHYDROGENASE (EC .2.1.11)        |                           |        |      |     |
| 1      |     |       |        |           |                 | l(ASA DEHYDROGENASE).   |                           |        |      |     |
| 1      | 271 | 1     | 3      | 1163      | gi 467091       | lhflX; B2235_C2_202 [Mycobacterium leprae]                                    | 64                        | 44     | 1161 |     |
| 1      | 280 | 1     | 173    | 1450      | gi 1303839      | lYqfR [Bacillus subtilis]   | 64                        | 43     | 1278 |     |
| 1      | 293 | 1     | 2532   | 1267      | gi 147345       | lprimosomal protein n' [Escherichia coli]                                     | 64                        | 45     | 1266 |     |
| 1      | 295 | 2     | 742    | 1488      | gi 459266       | lPotential membrane spanning protein [Staphylococcus hominis]                 | 64                        | 39     | 747  |     |
| 1      |     |       |        |           |                 | lpirS42932 S42932 potential membrane spanning protein - taphylococcus hominis |                           |        |      |     |
| 1      | 301 | 5     | 1625   | 1446      | gi 580835       | llysine decarboxylase [Bacillus subtilis]                                     | 64                        | 35     | 180  |     |
| 1      | 315 | 4     | 5064   | 3949      | gi 143396       | lquinol oxidase [Bacillus subtilis]   | 64                        | 45     | 1116 |     |
| 1      | 321 | 1     | 1264   | 635       | gi 710496       | ltranscriptional activator protein [Bacillus brevis]                          | 64                        | 41     | 630  |     |
| 1      | 333 | 5     | 4520   | 4239      | gi 1314295      | lORF2; putative 19 kDa protein [Listeria monocytogenes]                       | 64                        | 43     | 282  |     |
| 1      | 342 | 1     | 1      | 1         | 549             | gi 142940   | lftsA [Bacillus subtilis] | 64     | 38   | 549 |
| 1      | 353 | 3     | 2878   | 2324      | gi 537049       | lORF_0470 [Escherichia coli]  | 64                        | 44     | 555  |     |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop | match             | match gene name   | % sim | % ident | length |
|--------|-----|-------|------|-------------------|---|-------|---------|--------|
| ID     | ID  | (nt)  | (nt) | accession         |   |       |         | (nt)   |
| 379    | 2   | 827   | 3658 | lpir S25295 A328  | oxoglutarate dehydrogenase (lipoamide) (EC 1.2.4.2) - <i>Bacillus subtilis</i>    | 64    | 47      | 2832   |
| 404    | 6   | 4429  | 4839 | lpir A36933 A369  | diacylglycerol kinase homolog - <i>Streptococcus mutans</i>                       | 64    | 35      | 411    |
| 407    | 1   | 2020  | 1133 | lgi 969026        | OrfX [Bacillus subtilis]  | 64    | 41      | 888    |
| 425    | 1   | 1109  | 591  | lgi 1146177       | phosphotransferase system glucose-specific enzyme II [Bacillus subtilis]          | 64    | 44      | 519    |
| 443    | 6   | 4082  | 4798 | lgi 147309        | purine nucleoside phosphorylase [Escherichia coli]                                | 64    | 51      | 717    |
| 450    | 2   | 1035  | 1604 | lgi 606376        | lORF_0162 [Escherichia coli]  | 64    | 38      | 570    |
| 470    | 5   | 1680  | 6107 | lgi 1369948       | lhost interacting protein [Bacteriophage B1]                                      | 64    | 45      | 4428   |
| 486    | 4   | 1911  | 1471 | lgi 1205582       | [spermidine/putrescine transport system permease protein [Haemophilus influenzae] | 64    | 35      | 441    |
| 497    | 1   | 2217  | 1159 | lsp P36929 FMU_E  | lFMU PROTEIN.   | 64    | 38      | 1059   |
| 501    | 1   | 1     | 3    | lgi 142450        | lahRC protein [Bacillus subtilis]   | 64    | 38      | 408    |
| 514    | 1   | 1     | 3    | lgi 1204496       | [H. influenzae predicted coding region HI0238 [Haemophilus influenzae]            | 64    | 34      | 288    |
| 551    | 4   | 3162  | 3323 | lgi 1204511       | l bacterioferritin comigratory protein [Haemophilus influenzae]                   | 64    | 41      | 162    |
| 603    | 4   | 759   | 956  | lgi 755823        | lNADH dehydrogenase F [Streptogyna americana]                                     | 64    | 35      | 198    |
| 653    | 2   | 940   | 746  | lgi 1213234       | l dicarboxylic amino acids Dip5p permease [Saccharomyces cerevisiae]              | 64    | 41      | 195    |
| 660    | 3   | 3801  | 2257 | lsp P46133 YDAH_- | lHYPOTHETICAL PROTEIN IN OGT 5' REGION (FRAGMENT).                                | 64    | 39      | 1545   |
| 695    | 1   | 11    | 502  | lgi 1001383       | lhypothetical protein [Synchocystis sp.]  | 64    | 41      | 492    |
| 702    | 1   | 1     | 3    | lgi 142865        | lDNA primase [Bacillus subtilis]  | 64    | 46      | 750    |
| 826    | 1   | 1     | 339  | lgi 971336        | larginyl tRNA synthetase [Bacillus subtilis]                                      | 64    | 50      | 339    |
| 838    | 1   | 1831  | 917  | lgi 1354775       | lpfoS/R [Treponema pallidum]  | 64    | 41      | 915    |
| 864    | 3   | 675   | 944  | lgi 39833         | lcyclomaltodextrin glucanotransferase [Bacillus stearothermophilus]               | 64    | 47      | 270    |
| 887    | 1   | 3     | 677  | lgi 153002        | lenterotoxin type E precursor [Staphylococcus aureus] pir A28179 A28179           | 64    | 46      | 675    |
| 928    | 2   | 1172  | 963  | lgi 311976        | lenterotoxin E precursor - <i>Staphylococcus aureus</i> sp P12993 ETXE_STAAU      | 64    | 41      | 210    |
| 1049   | 2   | 800   | 606  | lgi 1049115       | lfibrinogen-binding protein - <i>Staphylococcus aureus</i>                        | 64    | 42      | 195    |
| 1067   | 2   | 999   | 748  | lgi 1151072       | lHhda precursor [Haemophilus ducreyi]   | 64    | 50      | 252    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop  | match<br>accession | match gene name   | % sim | % ident | length<br>(nt) |     |
|--------|-----|--------|-------|--------------------|---|-------|---------|----------------|-----|
| ID     | ID  | (nt)   | (nt)  |                    |   |       |         |                |     |
| 1120   | 1   | 50     | 202   | lgi 142439         | ATP-dependent nuclelease [Bacillus subtilis]  | 1     | 64      | 30             |     |
| 1125   | 1   | 751    | 377   | lgi 581648         | lepiB gene product [Staphylococcus epidermidis]   | 1     | 64      | 44             |     |
| 1688   | 1   | 402    | 214   | pir AO1365 TVM     | transforming protein K-ras - mouse  | 1     | 64      | 47             |     |
| 2472   | 1   | 2      | 358   | lgi 487282         | [Na+ -ATPase subunit J [Enterococcus hirae]   | 1     | 64      | 36             |     |
| 2989   | 1   | 520    | 356   | lgi 304134         | largC [Bacillus stearothermophilus]   | 1     | 64      | 50             |     |
| 3013   | 1   | 630    | 352   | lgi 551699         | cytochrome oxidase subunit I [Bacillus firmus]  | 1     | 64      | 51             |     |
| 3034   | 1   | 546    | 274   | lgi 1204349        | hypothetical protein (GB:DB09212_3) [Haemophilus influenzae]  | 1     | 64      | 50             |     |
| 3197   | 1   | 613    | 308   | lgi 1009366        | Respiratory nitrate reductase [Bacillus subtilis]   | 1     | 64      | 46             |     |
| 3303   | 1   | 90     | 362   | lgi 1107839        | lalginate lyase [Pseudomonas aeruginosa]  | 1     | 64      | 43             |     |
| 3852   | 2   | 82     | 288   | lgi 216746         | D-lactate dehydrogenase [Lactobacillus plantarum]   | 1     | 64      | 42             |     |
| 3868   | 1   | 1      | 312   | lgi 1149435        | lputative [Lactococcus lactis]  | 1     | 64      | 48             |     |
| 3918   | 1   | 660    | 331   | lgi 5532           | lactetyl-CoA acyltransferase [Yarrowia lipolytica]  | 1     | 64      | 46             |     |
| 4000   | 1   | 112    | 378   | lgi 984688         | lunknown [Saccharomyces cerevisiae]   | 1     | 64      | 44             |     |
| 4009   | 1   | 81     | 368   | lgi 39372          | lgrsB gene product [Bacillus brevis]  | 1     | 64      | 267            |     |
| 4166   | 1   | 2      | 349   | lgi 1149435        | lputative [Lactococcus lactis]  | 1     | 64      | 46             |     |
| 4366   | 1   | 2      | 307   | lgi 216267         | lORF2 [Bacillus megaterium]   | 1     | 64      | 44             |     |
| 4457   | 1   | 2      | 400   | lgi 1197667        | lvitellogenin [Anolis pulchellus]   | 1     | 64      | 43             |     |
| 11     | 3   | 1539   | 2438  | lgi 438228         | lORF C [Staphylococcus aureus]  | 1     | 63      | 32             |     |
| 24     | 7   | 5611   | 5423  | lgi 1369943        | lal gene product [Bacteriophage B1]   | 1     | 63      | 34             |     |
| 29     | 1   | 1      | 390   | lgi 467441         | expressed at the end of exponential growth under conditions in which the enzymes of the TCA cycle are repressed [Bacillus subtilis] lgi 467441<br>expressed at the end of exponential growth under conditions in which the enzymes of the TCA cycle are repressed Bacil | 1     | 63      | 43             | 189 |
| 31     | 6   | 6329   | 5712  | lgi 496943         |   | 1     | 63      | 47             |     |
| 44     | 23  | 114669 | 15019 | pir AO446 QQEC     |   | 1     | 63      | 36             |     |
| 48     | 6   | 4403   | 6250  | lgi 43498          |   | 1     | 63      | 42             |     |
| 50     | 5   | 3869   | 4738  | lgi 413967         | lipa-43d gene product [Bacillus subtilis]   | 1     | 63      | 43             |     |
| 53     | 6   | 6764   | 5742  | lgi 474176         | lregulator protein [Staphylococcus xylosus]   | 1     | 63      | 49             |     |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop   | match      | gene name   | % sim | % ident | length |
|--------|-----|--------|--------|------------|---|-------|---------|--------|
| ID     | ID  | (nt)   | (nt)   | accession  |   | (nt)  | (nt)    |        |
| 56     | 114 | 115880 | 117607 | gi 467409  | DNAPolymerase III subunit [Bacillus subtilis]                           | 1     | 63      | 44     |
| 57     | 111 | 7945   | 7376   | gi 537036  | ORF_0158 [Escherichia coli]   | 1     | 63      | 39     |
| 62     | 3   | 2479   | 2114   | gi 642656  | Unknown [Rhizobium meliloti]  | 1     | 63      | 41     |
| 70     | 8   | 6562   | 7353   | gi 1399821 | PhoC [Rhizobium meliloti]   | 1     | 63      | 46     |
| 75     | 2   | 223    | 927    | gi 149376  | HisG [Lactococcus lactis]   | 1     | 63      | 45     |
| 78     | 5   | 4912   | 4403   | gi 413950  | ipa-26d gene product [Bacillus subtilis]                                | 1     | 63      | 42     |
| 91     | 5   | 9076   | 7220   | gi 466997  | lmetH2; B2126_C1_157 [Mycobacterium leprae]                             | 1     | 63      | 41     |
| 91     | 8   | 110566 | 9448   | gi 1204344 | cystathione gamma-synthase [Haemophilus influenzae]                     | 1     | 63      | 45     |
| 120    | 1   | 21     | 1508   | gi 882657  | sulfite reductase (NADPH) flavoprotein beta subunit [Escherichia coli]  | 1     | 63      | 46     |
| 120    | 4   | 2722   | 4125   | gi 665994  | hypothetical protein [Bacillus subtilis]                                | 1     | 63      | 34     |
| 127    | 7   | 6064   | 7566   | gi 40162   | lmurE gene product [Bacillus subtilis]                                  | 1     | 63      | 44     |
| 149    | 6   | 2321   | 2106   | gi 148503  | dnak [Erysipelothrix rhusiopathiae]                                     | 1     | 63      | 40     |
| 149    | 126 | 104455 | 10170  | gi 4870    | ORF 2, has similarity to DNA polymerase [Saccharomyces kluyveri]        | 1     | 63      | 42     |
|        |     |        |        |            | r S159611S15961 hypothetical protein 2 - yeast (Saccharomyces yveri)    |       |         | 276    |
|        |     |        |        |            | plasmid PSK1  |       |         |        |
| 164    | 2   | 507    | 1298   | gi 145476  | CDP-diglyceride synthetase [Escherichia coli]                           | 1     | 63      | 44     |
| 166    | 6   | 9909   | 8164   | gi 151932  | fructose enzyme II [Rhodobacter capsulatus]                             | 1     | 63      | 41     |
| 169    | 4   | 1704   | 1886   | gi 1528886 | elongation factor Ts (tsf) [Spiroplasma citri]                          | 1     | 63      | 48     |
| 188    | 5   | 3145   | 2951   | gi 1334547 | GIY COI 114 grp IB protein [Podospora anserina]                         | 1     | 63      | 42     |
| 195    | 13  | 11767  | 12804  | gi 606100  | ORF_0335 [Escherichia coli]   | 1     | 63      | 40     |
| 201    | 2   | 607    | 2283   | gi 433534  | larginyl-tRNA synthetase [Corynebacterium glutamicum] pir A49936 A49936 | 1     | 63      | 46     |
| 206    | 14  | 115893 | 116489 | gi 580828  | arginine-tRNA ligase (EC 6.1.1.19) - orynebacterium glutamicum          | 1     | 63      | 49     |
| 220    | 5   | 17769  | 5766   | gi 216334  | N-acetyl-glutamate-gamma-semialdehyde dehydrogenase [Bacillus subtilis] | 1     | 63      | 42     |
| 221    | 1   | 74     | 907    | gi 677945  | seca protein [Bacillus subtilis]  | 1     | 63      | 42     |
| 227    | 3   | 944    | 1708   | gi 1510558 | cobyric acid synthase [Methanococcus jannaschii]                        | 1     | 63      | 46     |
| 261    | 2   | 804    | 1070   | gi 486511  | ORF YKR054C [Saccharomyces cerevisiae]                                  | 1     | 63      | 45     |
| 269    | 2   | 3606   | 1960   | gi 148221  | DNA-dependent ATPase, DNA helicase [Escherichia coli] pir JS0137 BVECQ  | 1     | 63      | 42     |
|        |     |        |        |            | recQ protein - Escherichia coli   |       |         | 1647   |

S. aureus – Putative coding regions of novel proteins similar to known proteins

| Contig | lORF | Start | Stop | match   | match gene name  | % sim   | % ident | length |     |
|--------|------|-------|------|---|--|---|---------|--------|-----|
| ID     | ID   | (nt)  | (nt) | accession   |  | (nt)  | (nt)    |        |     |
| 278    | 8    | 7417  | 6176 | gi 699273   | cystathionine gamma-synthase [Mycobacterium leprae] sp P46807 METB MYCLE CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9) O-SUCCINYLHOMOSERINE (THIOL)-LYASE . | 63  | 41      | 1242   |     |
| 287    | 2    | 738   | 1733 | gi 405133   | hypothetical protein [Bacillus subtilis]   | 63  | 38      | 996    |     |
| 295    | 1    | 2     | 748  | gi 1239983  | hypothetical protein [Bacillus subtilis]   | 63  | 41      | 747    |     |
| 328    | 3    | 2148  | 3134 | gi 45302  | carrier protein (AA 1 - 437) [Pseudomonas aeruginosa] ir S11497 S11497 branched-chain amino acid transport protein braB - pseudomonas aeruginosa         | 63  | 36      | 987    |     |
| 362    | 2    | 1626  | 1216 | sp P35136 SERA_ID-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95) (PGDH) . |  | 63  | 38      | 411    |     |
| 404    | 1    | 326   | 1051 | gi 1303816  | YqeZ [Bacillus subtilis]   | 63  | 35      | 726    |     |
| 405    | 3    | 2101  | 1715 | gi 1303914  | Yqhy [Bacillus subtilis]   | 63  | 42      | 387    |     |
| 406    | 1    | 451   | 227  | gi 142152   | sulfate permease (gtg start codon) [Synechococcus PCC6301] pir A30301 GRYCS7 sulfate transport protein - Synechococcus sp. PCC 7942                      | 63  | 43      | 225    |     |
| 415    | 2    | 1048  | 2718 | gi 1205402  | transport ATP-binding protein [Haemophilus influenzae]   | 63  | 41      | 1671   |     |
| 426    | 4    | 3575  | 2679 | gi 393268   | 29-kilodalton protein [Streptococcus pneumoniae] sp P42362 P29K_STRPN 29 KD MEMBRANE PROTEIN IN PSAA 5' REGION ORF1) .                                   | 63  | 39      | 897    |     |
| 505    | 3    | 1347  | 2195 | gi 1418999  | orf4 [Lactobacillus sake]  | 63  | 40      | 849    |     |
| 507    | 1    | 1     | 2    | 574   | gi 546917  | lcomK [Bacillus subtilis, E26, Peptide, 192 aa] | 63      | 35     | 573 |
| 562    | 2    | 146   | 1084 | gi 43985  | lnifS-like gene [Lactobacillus delbrueckii]  | 63  | 45      | 939    |     |
| 675    | 1    | 427   | 215  | gi 1510994  | lserine aminotransferase [Methanococcus jannaschii]  | 63  | 29      | 213    |     |
| 686    | 1    | 1     | 3    | 230   | gi 517356  | nitrate reductase (NADH) [Lotus japonicus]      | 63      | 52     | 228 |
| 701    | 1    | 3     | 392  | gi 881940   | NorQ protein [Paracoccus denitrificans]  | 63  | 41      | 390    |     |
| 720    | 1    | 1     | 2    | 400   | gi 47168   | open reading frame [Streptomyces lividans]      | 63      | 35     | 399 |
| 779    | 1    | 571   | 287  | gi 1261932  | lunkown [Mycobacterium tuberculosis]   | 63  | 41      | 285    |     |
| 907    | 1    | 1     | 22   | 321   | gi 149445  | lORF1 [Lactococcus lactis]                      | 63      | 27     | 300 |
| 972    | 1    | 794   | 399  | gi 1511235  | M. jannaschii predicted coding region MJ1232 [Methanococcus jannaschii]  | 63  | 27      | 396    |     |
| 1085   | 1    | 1154  | 618  | gi 11204277   | hypothetical protein [GB:U00019_14] [Haemophilus influenzae]   | 63  | 38      | 537    |     |
| 1094   | 1    | 3     | 542  | gi 799943   | lurea amidolyase [Bacillus subtilis]   | 63  | 39      | 540    |     |
| 1108   | 1    | 1     | 3    | 482   | pir S49892 S498 regulation protein - Bacillus subtilis   | 63  | 44      | 480    |     |
| 1113   | 1    | 1231  | 617  | gi 493017   | endocarditis specific antigen [Enterococcus faecalis]  | 63  | 45      | 615    |     |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop | match      | match gene name  |
|--------|-----|-------|------|------------|--|
| ID     | ID  | (nt)  | (nt) | accession  |  |
| 1300   | 1   | 1     | 3    | 695        | sp P33940 YQJH _ HYPOTHETICAL 54.3 KD PROTEIN IN ECO-ALKB INTERGENIC REGION.   |
| 1325   | 1   | 1     | 1    | 204        | lgi 928989 _ p100 protein [Borrelia burgdorferi]   |
| 1814   | 1   | 1     | 3    | 245        | lgi 1303914 _ YqhY [Bacillus subtilis]   |
| 2021   | 1   | 1     | 498  | 250        | pir C33496 C334 _ hisC homolog - Bacillus subtilis   |
| 2325   | 1   | 2     | 193  | lgi 436132 | product is similar to TnPa of transposon Tn554 from Staphylococcus ureus<br>  [Clostridium butyricum]  |
| 2335   | 1   | 1     | 1    | 195        | lgi 1184298 _ flagellar Ms-ring protein [Borrelia burgdorferi]   |
| 2406   | 1   | 1     | 451  | 227        | lgi 1041785 _ rhopty protein [Plasmodium yoelii]   |
| 2961   | 1   | 2     | 136  | 360        | lgi 312443 _ carbamoyl-phosphate synthase (glutamine-hydrolysing) [Bacillus aldoliticus]   |
| 2965   | 1   | 1     | 1    | 402        | lgi 1407784 _ orf-1; novel antigen [Staphylococcus aureus]   |
| 2987   | 1   | 1     | 583  | 293        | lgi 1224069 _ amidase [Moraxella catarrhalis]  |
| 2994   | 1   | 1     | 266  | 135        | lgi 836646 _ phosphoribosylformimino-praiaic ketoisomerase [Rhodobacter phaeooides]  |
| 3043   | 1   | 1     | 440  | 252        | lgi 1480237 _ phenylacetaldehyde dehydrogenase [Escherichia coli]  |
| 3078   | 1   | 1     | 609  | 400        | lgi 1487982 _ intrinsic membrane protein [Mycoplasma hominis]  |
| 3139   | 1   | 1     | 2    | 217        | lgi 439126 _ glutamate synthase (NADPH) [Azospirillum brasiliense] pir A49916 A49916<br>  glutamate synthase (NADPH) (EC 1.4.1.13) - zospirillum brasiliense   |
| 3625   | 1   | 1     | 793  | 398        | lgi 1623073 _ ORF360; putative [Bacteriophage LL-H]  |
| 3658   | 1   | 1     | 1    | 399        | lgi 1303697 _ YrKA [Bacillus subtilis]   |
| 3659   | 1   | 1     | 3    | 395        | lgi 1256135 _ YbbF [Bacillus subtilis]   |
| 3783   | 1   | 1     | 720  | 361        | lgi 1256902 _ Pyruvate decarboxylase isozyme 2 (Swiss Prot. accession number P16467)<br>  [Saccharomyces cerevisiae]   |
| 3900   | 1   | 1     | 338  | 171        | sp P10537 AMYB _ IBETA-AMYLASE (EC 3.2.1.2) (1,4-ALPHA-D-GLUCAN MALTOHYDROLASE).   |
| 4309   | 1   | 1     | 3    | 176        | lgi A37967 A379 _ neural cell adhesion molecule Ng-CAM precursor - chicken   |
| 4367   | 1   | 1     | 1    | 195        | lgi 1321932 _ Per6p gene product [Pichia pastoris]   |
| 4432   | 1   | 1     | 1    | 312        | lgi 1151259 _ HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii] pir A44756 A44756<br>  hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) Pseudomonas sp. |
| 4468   | 1   | 1     | 6    | 308        | lgi 1295464 _ ATPase [Lactococcus lactis]  |
| 33     | 1   | 3     | 1411 | 2400       | lgi 1153675 _ tagatose 6-P kinase [Streptococcus mutans]   |
| 36     | 1   | 9     | 5985 | 6218       | lgi 1490521 _ hMSH3 [Homo sapiens]   |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | ID     | Start  | Stop        | match<br>(nt) | match<br>(nt) | match gene name  | % sim | % ident | length | (nt) |
|--------|-----|--------|--------|-------------|---------------|---------------|--|-------|---------|--------|------|
| 37     | 1   | 1      | 2      | 721         | lgi 1107531   | lgi 1107531   | lceuE gene product [Campylobacter coli]  | 62    | 33      | 720    |      |
| 38     | 115 | 110912 | 11589  | lgi 1222058 |               |               | H. influenzae predicted coding region HIN1279 [Haemophilus influenzae]   | 62    | 38      | 678    |      |
| 38     | 125 | 119526 | 120329 | lgi 695280  |               |               | ORF2 [Alcaligenes eutrophus]   | 62    | 41      | 804    |      |
| 57     | 2   | 2      | 2523   | 1780        | lgi 471234    |               | orf1 [Haemophilus influenzae]  | 62    | 55      | 744    |      |
| 57     | 9   | 6646   | 6350   | lgi 508174  |               |               | EEIB domain of PTS-dependent Gat transport and phosphorylation Escherichia coli  | 62    | 35      | 297    |      |
| 58     | 1   | 1      | 2      | 559         | lgi 755152    |               | highly hydrophobic integral membrane protein [Bacillus subtilis] sp P442953 TAGG_BACSU TEICOIC ACID TRANSLOCATION PERMEASE PROTEIN AGG.                  | 62    | 34      | 558    |      |
| 67     | 10  | 8250   | 9014   | lgi 470683  |               |               | Shows similarity with ATP-binding proteins from other ABC-transport perons, Swiss Prot Accession Numbers P24137, P08007, P04285, P24136 Escherichia coli | 62    | 34      | 765    |      |
| 69     | 8   | 8315   | 7494   | lgi 46816   |               |               | lactVA 4 gene product [Streptomyces coelicolor]  | 62    | 44      | 822    |      |
| 80     | 3   | 1793   | 1320   | lgi 39993   |               |               | UDP-N-acetylglucosamine-D-glutamate ligase [Bacillus subtilis]   | 62    | 43      | 474    |      |
| 87     | 7   | 7034   | 9205   | lgi 217191  |               |               | 5'-nucleotidase precursor [Vibrio parahaemolyticus]  | 62    | 48      | 2172   |      |
| 100    | 3   | 4051   | 3089   | lgi 1511047 |               |               | phosphoglycerate dehydrogenase [Methanococcus jannaschii]  | 62    | 42      | 963    |      |
| 102    | 1   | 1      | 2      | 520         | lgi 153655    |               | mismatch repair protein [Streptococcus pneumoniae] pir C28667 C28667 DNA mismatch repair protein hexA - Streptococcus pneumoniae                         | 62    | 34      | 519    |      |
| 112    | 2   | 1466   | 1068   | lgi 153741  |               |               | ATP-binding protein [Streptococcus mutans]   | 62    | 37      | 603    |      |
| 114    | 7   | 6855   | 7562   | lgi 1204866 |               |               | L-fucose operon activator [Haemophilus influenzae]   | 62    | 38      | 708    |      |
| 116    | 4   | 6823   | 5633   | lgi 677947  |               |               | AppC [Bacillus subtilis]   | 62    | 37      | 1191   |      |
| 124    | 8   | 16855  | 6004   | lgi 853777  |               |               | product similar to E.coli PRF42 protein [Bacillus subtilis] pir S555438 S55438 ywke protein - Bacillus subtilis sp P45873 HEMK_BACSU                     | 62    | 44      | 852    |      |
| 148    | 1   | 24     | 554    | lgi 467456  |               |               | product similar to E.coli PRF42 protein [Bacillus subtilis] pir S555438 S55438 ywke protein - Bacillus subtilis sp P45873 HEMK_BACSU                     | 62    | 50      | 531    |      |
| 149    | 120 | 7591   | 6725   | lgi 1205807 |               |               | replicative DNA helicase [Haemophilus influenzae]  | 62    | 41      | 867    |      |
| 163    | 3   | 1503   | 1153   | lgi 40067   |               |               | lX gene product [Bacillus sphaericus]  | 62    | 42      | 351    |      |
| 164    | 115 | 114673 | 15632  | lgi 42219   |               |               | P35 gene product (AA 1 - 314) [Escherichia coli]   | 62    | 38      | 960    |      |
| 165    | 2   | 1166   | 1447   | lgi 403936  |               |               | phenylalanyl-tRNA synthetase alpha subunit (Gly294 variant) unidentified cloning vector]   | 62    | 38      | 282    |      |
| 166    | 2   | 2084   | 5089   | lgi 308861  |               |               | GTG start codon [Lactococcus lactis]   | 62    | 44      | 3006   |      |
| 171    | 1   | 1225   | 614    | lgi 1046053 |               |               | Hypothetical protein (SP:P32049) [Mycoplasma genitalium]   | 62    | 41      | 612    |      |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop   | match           | gene name  | % sim | % ident | length |
|--------|-----|--------|--------|-----------------|--|-------|---------|--------|
| ID     | ID  | (nt)   | (nt)   | accession       |  | (nt)  | (nt)    | (nt)   |
| 183    | 1   | 2521   | 1310   | gi 143045       | lhemY [Bacillus subtilis]  | 62    | 45      | 1212   |
| 200    | 1   | 1      | 3      | 1 956           | gi 142439<br>ATP-dependent nuclease [Bacillus subtilis]  | 62    | 32      | 954    |
| 237    | 2   | 935    | 1 1966 | gi 41695        | lhisC protein [Escherichia coli]   | 62    | 44      | 1032   |
| 261    | 3   | 4008   | 1 2605 | gi 143121       | lORF A; putative [Bacillus firmus]   | 62    | 42      | 1404   |
| 299    | 8   | 4477   | 4719   | gi 467441       | expressed at the end of exponential growth under conditions in which the<br>enzymes of the TCA cycle are repressed [Bacillus subtilis] gi 467441 | 62    | 47      | 243    |
| 304    | 6   | 5018   | 1 3819 | gi 153015       | lFemA protein [Staphylococcus aureus]  | 62    | 43      | 1200   |
| 324    | 1   | 2      | 1 262  | gi 142717       | cytochrome aa3 controlling protein [Bacillus subtilis] pir A33960 A33960<br>cta protein - Bacillus subtilis sp P12946 CTAA_BACSU CYTOCHROME AA3  | 62    | 30      | 261    |
| 325    | 2   | 269    | 1 1207 | gi 581088       | lMethionyl-tRNA formyltransferase [Escherichia coli]   | 62    | 39      | 939    |
| 332    | 6   | 4894   | 1 4631 | gi 1499960      | luridine 5'-monophosphate synthase [Methanococcus jannaschii]  | 62    | 36      | 264    |
| 355    | 1   | 1 2    | 1 370  | gi 145925       | lfecB [Escherichia coli]   | 62    | 32      | 369    |
| 365    | 8   | 6628   | 1 6804 | gi 413943       | lipa-19d gene product [Bacillus subtilis]  | 62    | 54      | 177    |
| 369    | 2   | 2744   | 1 1626 | pir A43577 A435 | lregulatory protein pf0R - Clostridium perfringens   | 62    | 42      | 1119   |
| 370    | 1   | 1 34   | 1 264  | gi 40665        | lbeta-glucosidase [Clostridium thermocellum]   | 62    | 37      | 231    |
| 415    | 3   | 1 2709 | 1 3176 | gi 1205401      | ltransport ATP-binding protein [Haemophilus influenzae]  | 62    | 35      | 468    |
| 429    | 1   | 1 1578 | 1 790  | gi 1046024      | lNa+ ATPase subunit J [Mycoplasma genitalium]  | 62    | 40      | 789    |
| 444    | 2   | 1 704  | 1 1369 | gi 581510       | lmodulation gene; integral membrane protein; homology to Rhizobium<br>leguminosarum nodI [Rhizobium loti]  | 62    | 37      | 666    |
| 477    | 1   | 2 751  | 1 1869 | pir A48440 A484 | lring-infected erythrocyte surface antigen 2, RESA-2 - Plasmodium falciparum   | 62    | 44      | 1119   |
| 485    | 1   | 1 241  | 1 1707 | gi 17934        | lbetaine aldehyde dehydrogenase [Beta vulgaris]  | 62    | 43      | 1467   |
| 487    | 3   | 1 1141 | 1 1311 | gi 149445       | lORF1 [Lactococcus lactis]   | 62    | 31      | 171    |
| 494    | 2   | 1 1134 | 1 1313 | gi 166835       | lribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana]   | 62    | 37      | 180    |
| 518    | 1   | 1 193  | 1 882  | gi 153491       | lO-methyltransferase [Streptomyces glaucescens]  | 62    | 39      | 690    |
| 534    | 2   | 1 369  | 1 2522 | gi 1480429      | lputative transcriptional regulator [Bacillus stearothermophilus]  | 62    | 35      | 2154   |
| 551    | 6   | 4371   | 1 4820 | gi 511113       | lferric uptake regulation protein [Campylobacter jejuni]   | 62    | 37      | 450    |
| 574    | 1   | 1 1    | 1 570  | gi 153000       | lenterotoxin B [Staphylococcus aureus]   | 62    | 43      | 570    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop | match       | match gene name   | % sim | % ident | length |
|--------|-----|-------|------|-------------|---|-------|---------|--------|
| ID     | ID  | (nt)  | (nt) | accession   |   |       |         | (nt)   |
| 590    | 2   | 344   | 1171 | lgi 40367   | ORFC [Clostridium acetobutylicum]   | 1     | 62      | 37     |
| 655    | 1   | 396   | 830  | lgi 147195  | lphnB protein [Escherichia coli]  | 1     | 62      | 44     |
| 656    | 1   | 2     | 478  | lgi 1205451 | cell division inhibitor [Haemophilus influenzae]  | 1     | 62      | 36     |
| 676    | 1   | 692   | 348  | lgi 1511613 | l-methyl coenzyme M reductase system, component A2 [Methanococcus jannaschii]                       | 1     | 62      | 36     |
| 687    | 1   | 493   | 248  | lgi 49272   | Asparaginase [Bacillus licheniformis]   | 1     | 62      | 48     |
| 700    | 2   | 267   | 944  | lgi 1205822 | hypothetical protein (GB:X5627_4) [Haemophilus influenzae]  | 1     | 62      | 40     |
| 840    | 2   | 1715  | 1041 | lgi 1045865 | [M. genitalium predicted coding region MG181 [Mycoplasma genitalium]]                               | 1     | 62      | 36     |
| 864    | 4   | 898   | 1491 | lgi 1144332 | deoxyuridine nucleotidohydrolase [Homo sapiens]   | 1     | 62      | 38     |
| 916    | 1   | 35    | 400  | lgi 413931  | lipa-7d gene product [Bacillus subtilis]  | 1     | 62      | 45     |
| 1071   | 1   | 1     | 771  | lgi 1510649 | aspartokinase I [Methanococcus jannaschii]  | 1     | 62      | 40     |
| 1084   | 1   | 19    | 609  | lgi 688011  | lAgX-1 antigen [human, infertile patient, testis, Peptide, 505 aa]                                  | 1     | 62      | 39     |
| 1103   | 1   | 3     | 203  | lgi 581261  | lORF homologous to E.coli metB [Herpetosiphon aurantiacus] pir S14030 S14030                        | 1     | 62      | 51     |
| 1217   | 1   | 463   | 233  | lgi 460025  | lORF2, putative [Streptococcus pneumoniae]  | 1     | 62      | 41     |
| 1533   | 1   | 644   | 414  | lgi 413968  | lipa-44d gene product [Bacillus subtilis]   | 1     | 62      | 48     |
| 1537   | 1   | 3     | 257  | lgi 1510641 | lalanY1-tRNA synthetase [Methanococcus jannaschii]  | 1     | 62      | 29     |
| 2287   | 1   | 3     | 161  | lgi 485956  | lmrpC gene product [Proteus mirabilis]  | 1     | 62      | 45     |
| 2386   | 1   | 3     | 245  | lgi 285708  | lntoxin component [Clostridium botulinum]   | 1     | 62      | 31     |
| 2484   | 1   | 331   | 167  | lgi 142092  | lDNA-repair protein (recA) [Anabaena variabilis]  | 1     | 62      | 35     |
| 2490   | 1   | 798   | 400  | lgi 581648  | lepiB gene product [Staphylococcus epidermidis]   | 1     | 62      | 42     |
| 3016   | 1   | 596   | 300  | lgi 710022  | luroporphyrinogen III [Bacillus subtilis]   | 1     | 62      | 51     |
| 3116   | 1   | 1     | 213  | lgi 466883  | lnifS; B1496_C2_193 [Mycobacterium leprae]  | 1     | 62      | 44     |
| 3297   | 1   | 823   | 413  | lgi 475715  | lactacyl coenzyme A acetyltransferase (thiolase) [Clostridium acetobutylicum]                       | 1     | 62      | 42     |
| 3609   | 1   | 31    | 276  | lgi 1408501 | homologous to N-acyl-L-amino acid amidohydrolase of Bacillus stearothermophilus [Bacillus subtilis] | 1     | 62      | 48     |
| 3665   | 2   | 584   | 402  | lgi 151259  | lHMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii] pir A44756 A44756                          | 1     | 62      | 40     |
|        |     |       |      |             | l hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) Pseudomonas sp.                                 | 1     |         | 183    |
| 3733   | 1   | 3     | 374  | lgi 1353197 | lthioredoxin reductase [Eubacterium acidaminophilum]  | 1     | 62      | 42     |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop   | match            | match gene name   | % sim | % ident | length |     |
|--------|-----|--------|--------|------------------|---|-------|---------|--------|-----|
| ID     | ID  | (nt)   | (nt)   | accession        |   |       |         | (nt)   |     |
| 3898   | 1   | 1      | 237    | gi 153675        | ltagatose 6-P kinase [Streptococcus mutans]                                 | 1     | 62      | 45     |     |
| 4027   | 1   | 1      | 283    | gi 143           | lhomologue to gene 30 (aa 1-59); putative [Bovine herpesvirus 4]            | 1     | 62      | 43     |     |
| 4109   | 1   | 1      | 727    | gi 41748         | lhsdM protein (AA 1-520) [Escherichia coli]                                 | 1     | 62      | 45     |     |
| 4303   | 1   | 1      | 303    | gi 1303813       | lyqEW [Bacillus subtilis]   | 1     | 62      | 43     |     |
| 4380   | 1   | 1      | 530    | gi 267           | lmevalonate pyrophosphate decarboxylase [Saccharomyces cerevisiae]          | 1     | 62      | 55     |     |
| 4494   | 1   | 1      | 256    | gi 510692        | lenterotoxin H [Staphylococcus aureus]                                      | 1     | 62      | 34     |     |
| 4598   | 1   | 1      | 411    | gi 763513        | lORF4; putative [Streptomyces violaceoruber]                                | 1     | 62      | 45     |     |
| 4624   | 1   | 1      | 222    | gi 41748         | lhsdM protein (AA 1-520) [Escherichia coli]                                 | 1     | 62      | 45     |     |
| 5      | 5   | 4288   | 3932   | gi 1928831       | lORF95; putative [Lactococcus lactis phage BKS-T]                           | 1     | 61      | 36     |     |
| 11     | 1   | 1      | 320    | lpir C33356 C333 | lprothymosin alpha homolog (clone 32) - human (fragment)                    | 1     | 61      | 33     |     |
| 16     | 11  | 110991 | 111938 | gi 1205391       | lhypothetical protein (SP:PP33995) [Haemophilus influenzae]                 | 1     | 61      | 44     |     |
| 32     | 1   | 1      | 283    | gi 11066504      | lexo-beta 1,3 glucanase [Cochliobolus carbonum]                             | 1     | 61      | 50     |     |
| 38     | 3   | 1      | 616    | gi 1107          | lglutamine transport ATP-binding protein Q [Methanococcus jannaschii]       | 1     | 61      | 41     |     |
| 45     | 4   | 3082   | 4038   | gi 11096886      | lProX [Bacillus subtilis]   | 1     | 61      | 45     |     |
| 48     | 8   | 1      | 7118   | gi 7504          | lORF2 [Clostridium perfringens]   | 1     | 61      | 33     |     |
| 51     | 1   | 9      | 4605   | gi 388269        | ltraC [Plasmid PAD1]  | 1     | 61      | 42     |     |
| 60     | 1   | 6      | 1689   | gi 1205893       | lhypothetical protein (GB:U00011_3) [Haemophilus influenzae]                | 1     | 61      | 32     |     |
| 62     | 1   | 9      | 5559   | gi 5122          | lNa/H antiporter system ORF2 [Bacillus alcalophilus]                        | 1     | 61      | 38     |     |
| 67     | 5   | 1      | 4330   | gi 466612        | lNika [Escherichia coli]  | 1     | 61      | 36     |     |
| 74     | 1   | 2      | 2400   | gi 1504          | lcarbamate kinase [Haemophilus influenzae]                                  | 1     | 61      | 40     |     |
| 85     | 1   | 1      | 2198   | gi 1101          | lamidophosphoribosyltransferase PurF [Rhizobium etli]                       | 1     | 61      | 41     |     |
| 86     | 4   | 1      | 1995   | gi 1582          | lM. jannaschii predicted coding region MJ1083 [Methanococcus jannaschii]    | 1     | 61      | 44     |     |
| 97     | 1   | 1      | 74     | gi 1518679       | lorf [Bacillus subtilis]  | 1     | 61      | 44     |     |
| 99     | 2   | 1      | 2454   | gi 1990          | lipa-34d gene product [Bacillus subtilis]                                   | 1     | 61      | 18     |     |
| 124    | 7   | 1      | 6223   | gi 5123          | lSimilar to Saccharomyces cerevisiae SUA5 protein [Bacillus subtilis]       | 61    | 46      | 1101   |     |
|        |     |        |        |                  | lpir 549358 S49358 ipc-29d protein - Bacillus subtilis sp P39153 YWLC_BACSU |       |         |        |     |
|        |     |        |        |                  | lHYPOTHETICAL 37.0 KD PROTEIN IN SPOIIR-GLYC NTERGENIC REGION.              |       |         |        |     |
| 125    | 4   | 1      | 1668   | gi 2531          | lORFA gene product [Chloroflexus aurantiacus]                               | 1     | 61      | 43     | 864 |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF ID | Start ID | Stop ID | match accession | match gene name   | % sim | % ident | length (nt) |
|--------|--------|----------|---------|-----------------|---|-------|---------|-------------|
| 132    | 1      | 1250     | 627     | pir PQ0259 PQ02 | hypothetical protein I - Enterococcus faecalis plasmid pAM-beta-1 (fragment)                                | 61    | 43      | 624         |
| 149    | 9      | 3617     | 3075    | gi 1144332      | deoxyuridine nucleotidohydrolase [Homo sapiens]   | 61    | 40      | 543         |
| 149    | 122    | 8690     | 7869    | gi 160047       | p101/acidic basic repeat antigen [Plasmodium falciparum] pira2932 A29232                                    | 61    | 35      | 822         |
| 168    | 3      | 1915     | 2361    | gi 1499694      | 101K malaria antigen precursor - Plasmodium aliciparum (strain Camp)  |       |         |             |
| 171    | 9      | 9675     | 7948    | gi 467446       | HIT protein, member of the HIT-family [Methanococcus jannaschii] (similar to SpovB [Bacillus subtilis])     | 61    | 41      | 447         |
| 174    | 3      | 1042     | 2340    | gi 216374       | glutaryl 7-ACA acylase precursor [Bacillus laterosporus]  | 61    | 38      | 1728        |
| 190    | 4      | 5034     | 4111    | gi 409286       | lbumrU [Bacillus subtilis]  | 61    | 37      | 924         |
| 216    | 1      | 2        | 190     | gi 415861       | leukaryotic initiation factor 2 beta (eIF-2 beta) [Oryctolagus cuniculus]                                   | 61    | 49      | 1299        |
| 227    | 7      | 4161     | 5048    | gi 216341       | lORF for methionine amino peptidase [Bacillus subtilis]   | 61    | 41      | 888         |
| 238    | 4      | 1959     | 3047    | gi 809543       | lCbrC protein [Erwinia chrysanthemi]  | 61    | 38      | 1089        |
| 247    | 1      | 2        | 694     | gi 537231       | lORF f579 [Escherichia coli]  | 61    | 38      | 693         |
| 247    | 2      | 678      | 1034    | gi 142226       | lchvD protein [Agrobacterium tumefaciens]   | 61    | 40      | 357         |
| 257    | 2      | 3523     | 2627    | gi 699379       | lg1vr-1 protein [Mycobacterium leprae]  | 61    | 40      | 897         |
| 268    | 2      | 3419     | 3051    | gi 40364        | lORFA1 [Clostridium acetobutylicum]   | 61    | 41      | 369         |
| 275    | 4      | 4621     | 4827    | gi 120488       | hypothetical protein (GP: M87049_57) [Haemophilus influenzae]   | 61    | 36      | 207         |
| 277    | 1      | 1        | 1845    | gi 784897       | lbeta-N-acetylhexosaminidase [Streptococcus pneumoniae] pira56390 A56390                                    | 61    | 45      | 1845        |
|        |        |          |         |                 | lmannosyl-glycoprotein ndo-beta-N-acetylglucosaminidase (EC 3.2.1.96)                                       |       |         |             |
|        |        |          |         |                 | lprecursor - treptococcus pneumoniae  |       |         |             |
| 278    | 9      | 8003     | 7032    | gi 467462       | lcysteine synthetase A [Bacillus subtilis]  | 61    | 43      | 972         |
| 278    | 10     | 9878     | 8535    | gi 1205919      | lNa <sup>+</sup> and Cl <sup>-</sup> dependent gamma-aminobutyric acid transporter [Haemophilus influenzae] | 61    | 38      | 1344        |
| 283    | 1      | 1        | 366     | gi 755607       | lpolyA polymerase [Bacillus subtilis]   | 61    | 36      | 366         |
| 288    | 2      | 1918     | 1496    | gi 388108       | lcell wall enzyme [Enterococcus faecalis]   | 61    | 43      | 423         |
| 291    | 1      | 86       | 334     | gi 454265       | lFBP3 [Petunia hybrida]   | 61    | 38      | 249         |
| 318    | 1      | 1104     | 694     | gi 290531       | lsimilar to beta-glucoside transport protein [Escherichia coli]   | 61    | 47      | 411         |
|        |        |          |         |                 | lsp P31451 PTIB ECOLI PTS SYSTEM, ARBUTIN-LIKE IIB COMPONENT  |       |         |             |
|        |        |          |         |                 | lPHOSPHOTRANSFERASE ENZYME II, B COMPONENT (EC 2.7.1.69)  |       |         |             |
| 330    | 2      | 1912     | 1190    | gi 1001805      | lhypothetical protein [Synchocystis sp.]  | 61    | 41      | 723         |

Table 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | l ORE | Start | Stop | match           | match gene name  | % sim | % ident | length |
|--------|-------|-------|------|-----------------|--|-------|---------|--------|
| ID     | ID    | (nt)  | (nt) | accession       |  | (nt)  | (nt)    | (nt)   |
| 385    | 2     | 1513  | 1025 | lgi 533098      | DnaD protein [Bacillus subtilis]   | 61    | 42      | 489    |
| 426    | 1     | 794   | 399  | lgi 1303853     | lYggF [Bacillus subtilis]  | 61    | 44      | 396    |
| 438    | 3     | 810   | 1421 | lgi 1293660     | AbsA2 [Streptomyces coelicolor]  | 61    | 36      | 612    |
| 454    | 1     | 1580  | 792  | lgi 733522      | phosphatidylinositol-4,5-diphosphate 3-kinase [Dictyostelium discoideum]   | 61    | 30      | 789    |
| 464    | 2     | 784   | 560  | lgi 1123120     | IC53B7.5 gene product [Caenorhabditis elegans]   | 61    | 38      | 225    |
| 470    | 8     | 6077  | 7357 | lgi 623073      | lORF360; putative [Bacteriophage LL-H]   | 61    | 47      | 1281   |
| 509    | 1     | 554   | 279  | lgi 467484      | lunknown [Bacillus subtilis]   | 61    | 45      | 276    |
| 555    | 3     | 1916  | 1296 | lgi 141800      | lanthranilate synthase glutamine amidotransferase [Acinetobacter alcoaceticus]   | 61    | 42      | 621    |
| 569    | 1     | 1711  | 857  | lgi 467090      | lB2235_C2_195 [Mycobacterium leprae]   | 61    | 47      | 855    |
| 585    | 2     | 961   | 803  | lsp P36686 SURE | lSURVIVAL PROTEIN SURE HOMOLOG (FRAGMENT).   | 61    | 33      | 159    |
| 592    | 3     | 1694  | 1422 | lgi 1221602     | limmunity repressor protein [Haemophilus influenzae]   | 61    | 32      | 273    |
| 603    | 1     | 43    | 357  | lgi 507738      | lHmp [Vibrio parahaemolyticus]   | 61    | 33      | 315    |
| 669    | 1     | 2467  | 1235 | lgi 1146243     | l22.4% identity with Escherichia coli DNA-damage inducible protein ...; lputative [Bacillus subtilis]  | 61    | 37      | 1233   |
| 675    | 3     | 805   | 1101 | lgi 4033373     | lglycerophosphoryl diester phosphodiesterase [Bacillus subtilis] lpir S37251 S37251 glycerophosphoryl diester phosphodiesterase - acillus subtilis | 61    | 36      | 297    |
| 703    | 1     | 1656  | 829  | lgi 537181      | lORF f470 [Escherichia coli]   | 61    | 32      | 828    |
| 728    | 1     | 1628  | 816  | lgi 806281      | lDNA polymerase I [Bacillus stearothermophilus]  | 61    | 39      | 813    |
| 821    | 1     | 61    | 318  | lgi 709992      | lhypothetical protein [Bacillus subtilis]  | 61    | 38      | 258    |
| 856    | 2     | 2313  | 1567 | lgi 609310      | lportal protein gp3 [Bacteriophage HK97]   | 61    | 40      | 747    |
| 923    | 1     | 1081  | 542  | lgi 143213      | lputative [Bacillus subtilis]  | 61    | 38      | 540    |
| 1124   | 1     | 59    | 370  | lgi 1107541     | lC33D9.8 [Caenorhabditis elegans]  | 61    | 26      | 312    |
| 1492   | 1     | 548   | 276  | lgi 1406397     | lunknown [Mycoplasma genitalium]   | 61    | 32      | 273    |
| 1602   | 1     | 46    | 318  | lgi 733522      | lphosphatidylinositol-4,5-diphosphate 3-kinase [Dictyostelium discoideum]  | 61    | 34      | 273    |
| 2500   | 1     | 577   | 290  | lgi 1045964     | lhypothetical protein (GB:U14003_297) [Mycoplasma genitalium]  | 61    | 31      | 288    |
| 2968   | 1     | 2     | 808  | lgi 397526      | lclumping factor [Staphylococcus aureus]   | 61    | 55      | 807    |
| 3076   | 1     | 3     | 248  | lgi 149373      | lORF 1 [Lactococcus lactis]  | 61    | 41      | 246    |

| Contig | lORF | Start | Stop | match      | % sim   | % ident | length |
|--------|------|-------|------|------------|---|---------|--------|
| ID     | ID   | (nt)  | (nt) | accession  |   |         | (nt)   |
| 3609   | 2    | 207   | 401  | gi 1408501 | homologous to N-acyl-L-amino acid amidohydrolase of <i>Bacillus stearothermophilus</i> [Bacillus subtilis]  | 61      | 39     |
| 3662   | 1    | 1477  | 740  | gi 1303813 | Yqew [Bacillus subtilis]  | 61      | 42     |
| 3672   | 1    | 2     | 442  | gi 784897  | beta-N-acetylhexosaminidase [Streptococcus pneumoniae] pir A56390 A56390<br>mannosyl-glycoprotein nbo-beta-N-acetylglucosaminidase (EC 3.2.1.96)<br>precursor - treptococcus pneumoniae | 61      | 50     |
| 3724   | 1    | 2     | 220  | gi 1009366 | Respiratory nitrate reductase [Bacillus subtilis]   | 61      | 41     |
| 3728   | 1    | 3     | 398  | gi 677943  | lAppD [Bacillus subtilis]   | 61      | 46     |
| 3884   | 1    | 3     | 401  | gi 784897  | beta-N-acetylhexosaminidase [Streptococcus pneumoniae] pir A56390 A56390<br>mannosyl-glycoprotein nbo-beta-N-acetylglucosaminidase (EC 3.2.1.96)<br>precursor - treptococcus pneumoniae | 61      | 47     |
| 3971   | 1    | 3     | 383  | gi 784897  | beta-N-acetylhexosaminidase [Streptococcus pneumoniae] pir A56390 A56390<br>mannosyl-glycoprotein nbo-beta-N-acetylglucosaminidase (EC 3.2.1.96)<br>precursor - treptococcus pneumoniae | 61      | 45     |
| 4038   | 1    | 661   | 359  | gi 1339950 | large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]  | 61      | 24     |
| 4041   | 1    | 546   | 274  | gi 413953  | lipa-29d gene product [Bacillus subtilis]   | 61      | 48     |
| 4047   | 1    | 1     | 402  | gi 528991  | unknown [Bacillus subtilis]   | 61      | 42     |
| 4102   | 1    | 1     | 345  | gi 976025  | lhrsA [Escherichia coli]  | 61      | 46     |
| 4155   | 1    | 1     | 336  | gi 784897  | beta-N-acetylhexosaminidase [Streptococcus pneumoniae] pir A56390 A56390<br>mannosyl-glycoprotein nbo-beta-N-acetylglucosaminidase (EC 3.2.1.96)<br>precursor - treptococcus pneumoniae | 61      | 50     |
| 4268   | 1    | 463   | 233  | gi 450688  | lhsdM gene of Ecoprr1 gene product [Escherichia coli] pir S38037 S38437 hsrdM<br>protein - Escherichia coli pir S09629 S09629 hypothetical protein A -<br>Escherichia coli (SUB 40-520) | 61      | 38     |
| 4374   | 1    | 542   | 273  | gi 784897  | beta-N-acetylhexosaminidase [Streptococcus pneumoniae] pir A56390 A56390<br>mannosyl-glycoprotein nbo-beta-N-acetylglucosaminidase (EC 3.2.1.96)  | 61      | 50     |
| 4389   | 1    | 2     | 172  | gi 147516  | ribokinase [Escherichia coli]   | 61      | 35     |
| 4621   | 1    | 2     | 268  | gi 784897  | beta-N-acetylhexosaminidase [Streptococcus pneumoniae] pir A56390 A56390<br>mannosyl-glycoprotein nbo-beta-N-acetylglucosaminidase (EC 3.2.1.96)<br>precursor - treptococcus pneumoniae | 61      | 47     |
| 4663   | 1    | 27    | 227  | gi 976025  | lhrsA [Escherichia coli]  | 61      | 50     |
| 4      | 6    | 6663  | 5536 | gi 1408501 | homologous to N-acyl-L-amino acid amidohydrolase of <i>Bacillus stearothermophilus</i> [Bacillus subtilis]  | 60      | 43     |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop   | match accession | match gene name  | % sim | % ident | length |
|--------|-----|--------|--------|-----------------|--|-------|---------|--------|
| ID     | ID  | (nt)   | (nt)   |                 |  | (nt)  | (nt)    | (nt)   |
| 11     | 6   | 3426   | 3725   | gi 410748       | ring-infested erythrocyte surface antigen [Plasmodium falciparum] - pir A25526 A25526 ring-infected erythrocyte surface antigen precursor - Plasmodium falciparum (strain FC27/Papua New Guinea) sp P13830 RESA_PLAFF - RING-INFECTED ERYTHROCYTE SURFACE ANTIGEN RE | 60    | 24      | 300    |
| 11     | 14  | 11035  | 10313  | gi 1217651      | lcarbonyl reductase (NADPH) [Rattus norvegicus]  | 60    | 28      | 723    |
| 16     | 12  | 11917  | 12930  | gi 1001453      | hypothetical protein [Synechocystis sp.]   | 60    | 37      | 1014   |
| 33     | 1   | 26     | 469    | gi 388109       | lregulatory protein [Enterococcus faecalis]  | 60    | 41      | 444    |
| 37     | 113 | 10814  | 9834   | gi 1336656      | Orf1 [Bacillus subtilis]   | 60    | 40      | 981    |
| 39     | 4   | 4364   | 4522   | gi 4872         | ORF 4 [Saccharomyces kluveri]  | 60    | 47      | 159    |
| 41     | 1   | 2047   | 1025   | gi 142822       | D-alanine racemase cds [Bacillus subtilis]   | 60    | 39      | 1023   |
| 43     | 4   | 2474   | 3607   | gi 468046       | para-nitrobenzyl esterase [Bacillus subtilis]  | 60    | 40      | 1134   |
| 44     | 10  | 6756   | 7769   | gi 414234       | lthiF [Escherichia coli]   | 60    | 52      | 1014   |
| 45     | 10  | 8874   | 9074   | gi 343949       | lvarl(40.0) [Saccharomyces cerevisiae]   | 60    | 44      | 201    |
| 56     | 118 | 127842 | 126430 | gi 468764       | lmocR gene product [Rhizobium meliloti]  | 60    | 35      | 1413   |
| 60     | 2   | 173    | 388    | gi 1303864      | lYqqQ [Bacillus subtilis]  | 60    | 33      | 216    |
| 63     | 2   | 357    | 1619   | gi 467124       | lureD; B229_C3_234 [Mycobacterium leprae]  | 60    | 43      | 1263   |
| 69     | 1   | 787    | 395    | gi 1518853      | lOafA [Salmonella typhimurium]   | 60    | 36      | 393    |
| 88     | 1   | 1      | 1188   | gi 1480429      | lputative transcriptional regulator [Bacillus stearothermophilus]  | 60    | 30      | 1188   |
| 92     | 6   | 4735   | 3881   | gi 349227       | ltransmembrane protein [Escherichia coli]  | 60    | 37      | 855    |
| 92     | 7   | 5996   | 4923   | gi 466613       | lnikB [Escherichia coli]   | 60    | 38      | 1074   |
| 93     | 1   | 949    | 476    | gi 1510925      | lcoenzyme F420-reducing hydrogenase, beta subunit [Methanococcus jannaschii]   | 60    | 27      | 474    |
| 96     | 6   | 7366   | 7578   | gi 972715       | laccessory protein [Carnobacterium piscicola]  | 60    | 30      | 213    |
| 98     | 6   | 3212   | 4069   | gi 467425       | lunknow [Bacillus subtilis]  | 60    | 42      | 858    |
| 102    | 10  | 7158   | 7430   | gi 143092       | lacetolactate synthase small subunit [Bacillus subtilis]   | 60    | 37      | 273    |
| 109    | 11  | 9127   | 10515  | gi 1255259      | lsp P37252 ILVN_BACSU ACETOLACTATE SYNTHASE SMALL SUBUNIT (EC .1.3.18) (AHAS) (ACETOHYDROXY-ACID SYNTHASE SMALL SUBUNIT) (ALS)   | 60    | 28      | 1389   |
| 109    | 12  | 110499 | 111656 | gi 141954       | lbeta-ketothiolase [Alcaligenes eutrophus]   | 60    | 41      | 1158   |
| 119    | 2   | 4630   | 3134   | gi 1524280      | lunknow [Mycobacterium tuberculosis]   | 60    | 45      | 1497   |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop  | match           | match gene name   | % sim | % ident | length |
|--------|-----|--------|-------|-----------------|---|-------|---------|--------|
| ID     | ID  | (nt)   | (nt)  | accession       |   | (nt)  |         | (nt)   |
| 121    | 9   | 6957   | 7646  | gi 1107529      | lceuC gene product [Campylobacter coli]   | 1     | 60      | 35     |
| 140    | 7   | 7704   | 6013  | gi 1146547      | lkdpa [Escherichia coli]  | 1     | 60      | 45     |
| 145    | 1   | 2      | 703   | gi 1146077      | lunknown [Mycobacterium tuberculosis]   | 1     | 60      | 23     |
| 150    | 3   | 2809   | 2216  | gi 1146230      | lputative [Bacillus subtilis]   | 1     | 60      | 40     |
| 157    | 2   | 1389   | 961   | gi 1303975      | lyqjX [Bacillus subtilis]   | 1     | 60      | 30     |
| 158    | 5   | 5125   | 4769  | gi 1449288      | lunknown [Mycobacterium tuberculosis]   | 1     | 60      | 36     |
| 159    | 1   | 511    | 257   | gi 580932       | lmurD gene product [Bacillus subtilis]  | 1     | 60      | 43     |
| 160    | 1   | 159    | 1187  | gi 1204532      | lhypothetical protein (GB:LI19201_29) [Haemophilus influenzae]  | 1     | 60      | 34     |
| 161    | 14  | 8249   | 7866  | gi 1496003      | lORF3; PepY; putative oligoendopeptidase based on homology with Lactococcus lactis PepF (GenBank Accession Number Z332522) [Caldicellulosiruptor saccharolyticus] | 1     | 60      | 34     |
| 172    | 3   | 1331   | 2110  | gi 485280       | l28.2 kDa protein [Streptococcus pneumoniae]  | 1     | 60      | 33     |
| 173    | 2   | 4082   | 2460  | gi 1524397      | lglycine betaine transporter OpD [Bacillus subtilis]  | 1     | 60      | 41     |
| 173    | 4   | 5963   | 4953  | gi 1100737      | lNADP dependent leukotriene b4 12-hydroxydehydrogenase [Sus scrofa]   | 1     | 60      | 44     |
| 198    | 1   | 3      | 995   | gi 413943       | lipa-19d gene product [Bacillus subtilis]   | 1     | 60      | 42     |
| 201    | 4   | 3641   | 4573  | sp P37028 YADT_ | lHYPOTHETICAL 29.4 KD PROTEIN IN HEML-PFS INTERGENIC REGION PRECURSOR.  | 1     | 60      | 37     |
| 203    | 3   | 3269   | 2415  | gi 927798       | lD9719_34p; CAI: 0.14 [Saccharomyces cerevisiae]  | 1     | 60      | 43     |
| 206    | 9   | 112234 | 12515 | sp P37347 YECD_ | lHYPOTHETICAL 21.8 KD PROTEIN IN ASPS' REGION.  | 1     | 60      | 47     |
| 212    | 4   | 1213   | 1410  | gi 332711       | lhemagglutinin-neuraminidase fusion protein [Human parainfluenza virus 3]   | 1     | 60      | 34     |
| 214    | 1   | 65     | 1153  | gi 1204366      | lhypothetical protein (GB:U14003_130) [Haemophilus influenzae]  | 1     | 60      | 36     |
| 237    | 1   | 2      | 937   | gi 149377       | lHisD [Lactococcus lactis]  | 1     | 60      | 40     |
| 241    | 6   | 5696   | 4998  | gi 1046160      | lhypothetical protein (GB:U00021_5) [Mycoplasma genitalium]   | 1     | 60      | 37     |
| 260    | 6   | 5919   | 6485  | gi 431950       | lsimilar to a B.subtilis gene (GB: BACHEMEHY_5) [Clostridium asteurianum]   | 1     | 60      | 35     |
| 264    | 1   | 2432   | 1218  | gi 397526       | lclumping factor [Staphylococcus aureus]  | 1     | 60      | 53     |
| 267    | 1   | 3      | 1409  | gi 148316       | lNaH-antporter protein [Enterococcus hirae]   | 1     | 60      | 27     |
| 275    | 3   | 3804   | 4595  | pir F36889 F368 | lleuD 3'-region hypothetical protein - Lactococcus lactis subsp. lactis (strain IL1403)   | 1     | 60      | 35     |
| 291    | 3   | 860    | 1198  | gi 1208889      | lcoded for by C. elegans cDNA yk130e12.5; contains C2H2-type zinc fingers [Caenorhabditis elegans]  | 1     | 60      | 33     |

## S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop | match           | match gene name  | % sim | % ident | length |
|--------|-----|-------|------|-----------------|--|-------|---------|--------|
| ID     | ID  | (nt)  | (nt) | accession       |  | (nt)  |         | (nt)   |
| 307    | 6   | 3421  | 3176 | gi 1070014      | lprotein-dependent [Bacillus subtilis]   | 1     | 60      | 36     |
| 316    | 8   | 4957  | 5823 | gi 413952       | lipa-28d gene product [Bacillus subtilis]  | 1     | 60      | 41     |
| 328    | 4   | 2996  | 3484 | gi 1204484      | membrane-associated component, branched amino acid transport system [Haemophilus influenzae] | 1     | 60      | 39     |
| 332    | 5   | 4887  | 4363 | gi 1205449      | lcolicin V production protein (pur regulon) [Haemophilus influenzae]                         | 1     | 60      | 37     |
| 357    | 1   | 1062  | 532  | gi 887842       | lsingle-stranded DNA-specific exonuclease [Escherichia coli]                                 | 1     | 60      | 41     |
| 375    | 2   | 96    | 362  | gi 4857         | ladenylyl cyclase gene product [Saccharomyces kluveri] r JQ1145 CYBYK                        | 1     | 60      | 47     |
| 397    | 1   | 66    | 416  | gi 709999       | ladenylyl cyclase (EC 4.6.1.1) - yeast ccharomyces kluveri)                                  | 1     | 60      | 37     |
| 409    | 1   | 2     | 163  | gi 499700       | lGlucarate dehydratase [Bacillus subtilis]   | 1     | 60      | 35     |
| 453    | 4   | 914   | 1237 | gi 1196899      | lglycogen phosphorylase [Saccharomyces cerevisiae]   | 1     | 60      | 36     |
| 453    | 7   | 3838  | 3620 | sp P12222 YCF1  | lunknown protein [Staphylococcus aureus]   | 1     | 60      | 31     |
| 470    | 2   | 622   | 945  | pir S30782 S307 | lHYPOTHETICAL 226 KD PROTEIN (ORF 1901).   | 1     | 60      | 219    |
| 500    | 1   | 118   | 606  | gi 467407       | lintegrin homolog - yeast (Saccharomyces cerevisiae)   | 1     | 60      | 31     |
| 503    | 3   | 752   | 982  | gi 167835       | lmyosin heavy chain [Dictyostelium discoideum]   | 1     | 60      | 36     |
| 505    | 4   | 2238  | 3563 | gi 1510732      | lNADH oxidase [Methanococcus jannaschii]   | 1     | 60      | 26     |
| 523    | 1   | 3     | 1043 | gi 143331       | lalkaline phosphatase regulatory protein [Bacillus subtilis]                                 | 1     | 60      | 41     |
| 543    | 1   | 1     | 1    | gi 1511103      | lpirl A27650 A27650 regulatory protein phoR - Bacillus subtilis                              | 1     | 60      | 34     |
| 545    | 1   | 1     | 1    | gi 1498192      | lsp P23545 PHOR_BACSU ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN HOR (EC 2.7.3.-).        | 1     | 60      | 1326   |
| 556    | 1   | 2     | 1054 | gi 1477402      | lcobalt transport ATP-binding protein O [Methanococcus jannaschii]                           | 1     | 60      | 40     |
| 578    | 1   | 974   | 489  | gi 1205129      | lputative [Pseudomonas aeruginosa]   | 1     | 60      | 40     |
| 594    | 1   | 1     | 624  | gi 1212755      | ltex gene product [Bordetella pertussis]   | 1     | 60      | 42     |
| 604    | 1   | 3     | 530  | gi 145925       | ladenylyl cyclase [Aeromonas hydrophila]   | 1     | 60      | 45     |
| 620    | 1   | 926   | 465  | gi 1205483      | lbicyclomycin resistance protein [Haemophilus influenzae]                                    | 1     | 60      | 42     |
| 630    | 2   | 871   | 1122 | gi 1486242      | lunknown [Bacillus subtilis]   | 1     | 60      | 41     |
| 645    | 2   | 574   | 425  | gi 1205136      | lserine hydroxymethyltransferase (serine methylase) [Haemophilus influenzae]                 | 1     | 60      | 28     |

## S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop | match           | match gene name  |
|--------|-----|-------|------|-----------------|--|
| ID     | ID  | (nt)  | (nt) | accession       |  |
| 684    | 1   | 1082  | 843  | gi 1205538      | hypothetical protein (GB:U14003_302) [Haemophilus influenzae]                        |
| 786    | 1   | 967   | 485  | gi 1402944      | lorfM1 gene product [Bacillus subtilis]  |
| 844    | 1   | 588   | 346  | gi 790943       | lurea amidolyase [Bacillus subtilis]   |
| 851    | 1   | 1     | 1    | gi 159661       | IGMP reductase [Ascaris lumbricoides]  |
| 871    | 1   | 1746  | 874  | gi 11001493     | hypothetical protein [Synechocystis sp.]   |
| 896    | 1   | 1558  | 839  | gi 604926       | NADH dehydrogenase, subunit 5 [Schizopyillum commune] sp P50368 NU5M_SCHCO           |
| 908    | 2   | 448   | 753  | gi 662880       | NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 6.5.3).                                   |
| 979    | 1   | 2     | 595  | gi 1429255      | Inovel hemolytic factor [Bacillus cereus]  |
| 1078   | 1   | 669   | 502  | gi 581055       | putative; orf1 [Bacillus subtilis]   |
| 1112   | 1   | 1150  | 620  | gi 407885       | inner membrane copper tolerance protein [Escherichia coli] gi 871029                 |
| 1135   | 1   | 484   | 275  | gi 1171407      | inner membrane copper tolerance protein [Escherichia coli] gi 871029                 |
| 1146   | 1   | 17    | 562  | gi 1239981      | disulphide isomerase like protein [Escherichia coli] pir S47295 S47295               |
| 1291   | 1   | 716   | 360  | pir S57530 S575 | carboxyl esterase - Acinetobacter calcoaceticus                                      |
| 1332   | 1   | 336   | 169  | gi 1222056      | laminotransferase [Haemophilus influenzae]   |
| 1429   | 1   | 3     | 146  | gi 1205619      | ferritin like protein [Haemophilus influenzae]                                       |
| 1722   | 1   | 570   | 286  | gi 240052       | dihydroflavonol-4-reductase, DFR [Hordeum vulgare=barley, cv. Gula, ep tide, 354 aa] |
| 2350   | 1   | 385   | 200  | gi 497626       | ORF 1 [Plasmid pAQ1]   |
| 2936   | 1   | 519   | 310  | gi 508981       | prephenate dehydratase [Bacillus subtilis]   |
| 3027   | 1   | 568   | 302  | gi 1146199      | putative [Bacillus subtilis]   |
| 3084   | 1   | 20    | 208  | gi 1407784      | orf-1; novel antigen [Staphylococcus aureus]   |
| 3155   | 1   | 2     | 226  | gi 1046997      | cytadherence-accessory protein [Mycoplasma genitalium]                               |
| 3603   | 1   | 368   | 186  | gi 510108       | mitochondrial long-chain enoyl-CoA hydratase/3-hydroxyacyl-CoA hydrogenase           |
| 3665   | 1   | 486   | 244  | gi 151259       | alpha subunit [Rattus norvegicus]  |
| 3747   | 1   | 3     | 146  | gi 474192       | HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii] pir A44756 A44756            |
|        |     |       |      |                 | hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) Pseudomonas sp.                    |
|        |     |       |      |                 | iucc gene product [Escherichia coli]   |

| Contig | ORF | Start  | Stop   | match           | match gene name   | % sim | % ident | length |
|--------|-----|--------|--------|-----------------|---|-------|---------|--------|
| ID     | ID  | (nt)   | (nt)   | accession       |   | (nt)  | (nt)    |        |
| 3912   | 1   | 3      | 335    | gi 1488695      | novel antigen; orf-2 [Staphylococcus aureus]                                      | 60    | 44      | 333    |
| 4072   | 1   | 3      | 272    | gi 405879       | lyeH [Escherichia coli]   | 60    | 33      | 270    |
| 4134   | 1   | 510    | 352    | gi 780656       | chemoreceptor protein [Rhizobium leguminosarum bv. viciae] gi 780656              | 60    | 28      | 159    |
| 4207   | 2   | 677    | 402    | gi 602031       | similar to trimethylamine DH [Mycoplasma capricolum] pir S49950 S49950            | 60    | 41      | 276    |
|        |     |        |        |                 | probable trimethylamine dehydrogenase (EC .5.99.7) - Mycoplasma capricolum        |       |         |        |
|        |     |        |        |                 | (SGC3) (fragment)   |       |         |        |
| 4243   | 1   | 127    | 324    | gi 899317       | peptidase synthetase module [Microcystis aeruginosa] pir S49111 S49111            | 60    | 42      | 198    |
|        |     |        |        |                 | probable amino acid activating domain - icrocystis aeruginosa (fragment)          |       |         |        |
|        |     |        |        |                 | {SUB 144-528}   |       |         |        |
| 4310   | 1   | 624    | 313    | gi 508980       | lpheB [Bacillus subtilis]   | 60    | 28      | 312    |
| 4345   | 1   | 343    | 173    | gi 510108       | mitochondrial long-chain enoyl-CoA hydratase/3-hydroxycyl-CoA enoyl-CoA hydratase | 60    | 42      | 171    |
|        |     |        |        |                 | alpha-subunit [Rattus norvegicus]   |       |         |        |
| 4382   | 1   | 498    | 280    | gi 47382        | acyl-CoA-dehydrogenase [Streptomyces purpurascens]                                | 60    | 48      | 219    |
| 4474   | 1   | 53     | 223    | gi 510108       | mitochondrial long-chain enoyl-CoA hydratase/3-hydroxycyl-CoA enoyl-CoA hydratase | 60    | 42      | 171    |
|        |     |        |        |                 | alpha-subunit [Rattus norvegicus]   |       |         |        |
| 23     | 4   | 4518   | 3523   | gi 426446       | lVipB protein [Salmonella typhi]  | 59    | 39      | 996    |
| 33     | 2   | 707    | 1483   | pir S48604 S486 | hypothetical protein - Mycoplasma capricolum (SGC3) (fragment)                    | 59    | 33      | 777    |
| 33     | 5   | 4651   | 5853   | gi 6721         | F59B2.3 [Caenorhabditis elegans]  | 59    | 33      | 1203   |
| 37     | 2   | 3228   | 2299   | gi 142833       | ORF2 [Bacillus subtilis]  | 59    | 37      | 930    |
| 38     | 121 | 116784 | 116593 | gi 912576       | BiP [Phaeodactylum tricornutum]   | 59    | 40      | 192    |
| 52     | 3   | 2648   | 2349   | gi 536972       | ORF_090a [Escherichia coli]   | 59    | 44      | 300    |
| 54     | 112 | 114181 | 113402 | gi 483940       | transcription regulator [Bacillus subtilis]                                       | 59    | 37      | 780    |
| 57     | 3   | 4397   | 3339   | gi 508176       | Gat-1-P-DH, NAD dependent [Escherichia coli]                                      | 59    | 40      | 1059   |
| 66     | 1   | 986    | 495    | gi 1303901      | Yqnt [Bacillus subtilis]  | 59    | 34      | 492    |
|        |     |        |        |                 | nikC [Escherichia coli]   | 59    | 37      | 909    |
| 67     | 7   | 6552   | 7460   | gi 912461       | PhoD precursor [Rhizobium meliloti]   | 59    | 46      | 984    |
| 70     | 7   | 5383   | 6366   | gi 1399822      | unknown, similar to E.coli cardiolipin synthase [Bacillus subtilis]               | 59    | 39      | 1449   |
| 78     | 1   | 1      | 1449   | gi 971345       | sp P45860 YWE_BACSU HYPOTHETICAL 58.2 PROTEIN IN NARI-ACDA NTERGENIC REGION.      |       |         |        |
| 82     | 10  | 114329 | 115534 | gi 490328       | LORF F [unidentified]   | 59    | 44      | 1206   |

## S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | ID     | Start  | Stop        | match  | gene name  | % sim | % ident | length |
|--------|-----|--------|--------|-------------|--|--|-------|---------|--------|
| ID     | ID  | (nt)   | (nt)   | accession   |  |  |       |         | (nt)   |
| 89     | 2   | 1602   | 958    | lgi 642801  | lunknow  | [ <i>Saccharomyces cerevisiae</i> ]                    | 1     | 59      | 32     |
| 96     | 4   | 4940   | 5473   | lgi 1333802 | protein of unknown function  | [ <i>Rhodobacter capsulatus</i> ]                      | 1     | 59      | 33     |
| 98     | 1   | 1      | 2      | 820         | lgi 467421   | similar to <i>B. subtilis</i> DnaK [Bacillus subtilis] | 1     | 59      | 34     |
| 119    | 1   | 166    | 1557   | lgi 143122  | ORF B; putative  | [ <i>Bacillus firmus</i> ]                             | 1     | 59      | 36     |
| 120    | 10  | 6214   | 6756   | lgi 15354   | ORF 55.9 [Bacteriophage T4]  |  | 1     | 59      | 39     |
| 120    | 116 | 12476  | 13510  | lgi 1086575 | lBetaA [Rhizobium meliloti]  |  | 1     | 59      | 44     |
| 123    | 1   | 386    | 195    | lgi 984737  | catalase   | [ <i>Campylobacter jejuni</i> ]                        | 1     | 59      | 38     |
| 130    | 1   | 370    | 645    | lgi 1256634 | 25.8% identity over 120 aa with the <i>Synenococcus</i> sp. MpeV protein; putative | [ <i>Bacillus subtilis</i> ]                           | 1     | 59      | 31     |
| 131    | 4   | 5278   | 5712   | lgi 1510655 | hypothetical protein (SP:R42297) [Methanococcus jannaschii]                        |  | 1     | 59      | 39     |
| 164    | 1   | 1      | 3      | 509         | lgi 1001342  | hypothetical protein [Synechocystis sp.]               | 1     | 59      | 41     |
| 164    | 4   | 1529   | 2821   | lgi 1205165 | hypothetical protein (SP:P37764) [Haemophilus influenzae]                          |  | 1     | 59      | 35     |
| 164    | 19  | 119643 | 121376 | lgi 1001381 | hypothetical protein [Synechocystis sp.]   |  | 1     | 59      | 34     |
| 173    | 3   | 4727   | 3717   | lgi 1184121 | auxin-induced protein [Vigna radiata]  |  | 1     | 59      | 50     |
| 179    | 2   | 2218   | 1688   | lgi 143036  | unidentified gene product [Bacillus subtilis]                                      |  | 1     | 59      | 33     |
| 195    | 112 | 12669  | 11503  | lgi 762778  | NifS gene product [Anabaena azollae]   |  | 1     | 59      | 41     |
| 201    | 5   | 4702   | 5670   | lgi 1510240 | hemin permease [Methanococcus jannaschii]  |  | 1     | 59      | 32     |
| 201    | 7   | 5719   | 6315   | lgi 1511456 | [M. jannaschii predicted coding region MJ1437 [Methanococcus jannaschii]           |  | 1     | 59      | 34     |
| 209    | 1   | 102    | 461    | lgi 1204666 | hypothetical protein (GB:X3124_53) [Haemophilus influenzae]                        |  | 1     | 59      | 42     |
| 214    | 3   | 1050   | 2234   | lgi 551531  | 1,2-nitropropane dioxygenase [Williopsis saturnus]                                 |  | 1     | 59      | 36     |
| 214    | 5   | 3293   | 4135   | lgi 1303709 | YrkJ [Bacillus subtilis]   |  | 1     | 59      | 32     |
| 217    | 2   | 3381   | 2167   | lgi 290489  | ldfp (CG Site No. 18430) [Escherichia coli]  |  | 1     | 59      | 44     |
| 237    | 5   | 3078   | 3785   | lgi 149382  | HisA [Lactococcus lactis]  |  | 1     | 59      | 38     |
| 251    | 2   | 376    | 960    | lgi 1303791 | YqeJ [Bacillus subtilis]   |  | 1     | 59      | 34     |
| 286    | 1   | 1621   | 812    | lgi 146551  | transmembrane protein (kdpD) [Escherichia coli]                                    |  | 1     | 59      | 31     |
| 316    | 5   | 4978   | 3860   | lgi 405879  | lyeH [Escherichia coli]  |  | 1     | 59      | 32     |
| 370    | 3   | 600    | 761    | lgi 1303794 | YqeM [Bacillus subtilis]   |  | 1     | 59      | 35     |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop | match           | match gene name  |
|--------|-----|-------|------|-----------------|--|
| ID     | ID  | (nt)  | (nt) | accession       | (nt)   |
| 382    | 1   | 1009  | 506  | gi 547513       | orf3 [Haemophilus influenzae]  |
| 391    | 3   | 1620  | 1273 | gi 152901       | ORF 3 [Spirochaeta aurantia]   |
| 406    | 3   | 2805  | 1705 | gi 709992       | hypothetical protein [Bacillus subtilis]   |
| 426    | 5   | 3802  | 3245 | gi 1204610      | Iron(III) dicitrato transport ATP-binding protein FECE [Haemophilus influenzae]        |
| 429    | 2   | 1513  | 1148 | gi 1064809      | homologous to sp:HTRA_ECOLI [Bacillus subtilis]  |
| 460    | 2   | 708   | 1301 | gi 466882       | ppsl; B1496_C2_189 [Mycobacterium leprae]  |
| 461    | 4   | 2212  | 3135 | gi 1498295      | 'homoserine kinase homolog [Streptococcus pneumoniae]                                  |
| 473    | 1   | 2929  | 1607 | gi 147989       | trigger factor [Escherichia coli]  |
| 480    | 8   | 5862  | 6110 | gi 1205311      | (3R)-hydroxymyristol acyl carrier protein dehydrase [Haemophilus influenzae]           |
| 521    | 1   | 14    | 1354 | pir A25620 A256 | Staphylococcus aureus (fragment)   |
| 534    | 4   | 2994  | 4073 | gi 153746       | mannitol-phosphate dehydrogenase [Streptococcus mutans] pir C44798 C44798              |
| 535    | 1   | 1     | 954  | gi 1469939      | group B oligopeptidase PepB [Streptococcus agalactiae]                                 |
| 551    | 3   | 2836  | 3186 | gi 1204511      | bacterioferritin comigratory protein [Haemophilus influenzae]                          |
| 573    | 2   | 449   | 940  | gi 386681       | ORF YAL022 [Saccharomyces cerevisiae]  |
| 650    | 1   | 5     | 748  | gi 396400       | similar to eukaryotic Na <sup>+</sup> /H <sup>+</sup> exchangers [Escherichia coli]    |
| 664    | 1   | 566   | 285  | gi 11262748     | sp P32703 YJCE_ECOLI HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS NTERGENIC REGION (O549). |
| 670    | 1   | 3     | 455  | gi 1122758      | LukF-PV like component [Staphylococcus aureus]   |
| 674    | 3   | 543   | 929  | gi 293033       | Integrase [Bacteriophage phi-IC3]  |
| 758    | 1   | 349   | 176  | gi 1500472      | M. jannaschii predicted coding region MJ1577 [Methanococcus jannaschii]                |
| 771    | 2   | 2270  | 1461 | gi 522150       | bromoperoxidase BPO-A1 [Streptomyces aureofaciens] sp P33912 BPA1_STRAU                |
|        |     |       |      |                 | NON-HAEM BROMOPEROXIDASE BPO-A1 (EC 1.11.1.-) BROMIDE PEROXIDASE (BPO1).               |
|        |     |       |      |                 | (SUB 2-275)  |
| 825    | 1   | 2191  | 1097 | gi 397526       | clumping factor [Staphylococcus aureus]  |
| 1052   | 2   | 1094  | 723  | gi 289262       | lcomE ORF3 [Bacillus subtilis]   |
| 1152   | 1   | 373   | 188  | gi 1276668      | ORF238 gene product [Porphyra purpurea]  |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop  | match     | match gene name | % sim   | % ident | length |
|--------|-----|-------|-------|-----------|-----------------|---|---------|--------|
| ID     | ID  | (nt)  | (nt)  | accession |                 | (nt)  | (nt)    |        |
| 1198   | 1   | 1     | 492   | 247       | gi 142439       | ATP-dependent nuclelease [Bacillus subtilis]  | 1       | 59     |
| 1441   | 1   | 1     | 468   | 235       | gi 1045942      | glycyl-tRNA synthetase [Mycoplasma genitalium]  | 1       | 59     |
| 2103   | 1   | 1     | 1     | 186       | gi 1459250      | triacylglycerol lipase [Galactomyces geotrichum]  | 1       | 59     |
| 2205   | 1   | 1     | 793   | 398       | gi 1303794      | YqEM [Bacillus subtilis]  | 1       | 59     |
| 2578   | 1   | 1     | 484   | 284       | gi 258003       | insulin-like growth factor binding protein complex acid-labile subunit [rats, liver, Peptide, 603 aa]   | 1       | 59     |
| 2967   | 1   | 2     | 145   | 348       | gi 1212730      | YqHK [Bacillus subtilis]  | 1       | 59     |
| 3012   | 1   | 1     | 3     | 248       | gi 773571       | neurofilament protein NF70 [Helix aspersa]  | 1       | 59     |
| 3544   | 1   | 1     | 3     | 401       | gi 1055218      | crotonase [Clostridium acetobutylicum]  | 1       | 59     |
| 3548   | 1   | 1     | 3     | 401       | gi 1055218      | crotonase [Clostridium acetobutylicum]  | 1       | 59     |
| 3580   | 1   | 1     | 698   | 351       | gi 1055218      | crotonase [Clostridium acetobutylicum]  | 1       | 59     |
| 3720   | 1   | 1     | 722   | 363       | gi 1408494      | homologous to penicillin acylase [Bacillus subtilis]  | 1       | 59     |
| 4171   | 1   | 1     | 3     | 296       | gi 1055218      | crotonase [Clostridium acetobutylicum]  | 1       | 59     |
| 4305   | 1   | 1     | 618   | 310       | gi 1524193      | lunknow [Mycobacterium tuberculosis]  | 1       | 59     |
| 18     | 1   | 1     | 1242  | 622       | gi 146913       | [N-acetylglucosamine transport protein [Escherichia coli] pir B29895 WQEC2N phosphotransferase system enzyme II (EC 7.1.69), N-acetylglucosamine-specific - Escherichia coli sp P09323 PTAA_ECOLI PTS SYSTEM, N-ACETYLGLUCOSAMINE-SPECIFIC LIABC COMPONENT (ELIA) | 1       | 58     |
| 20     | 1   | 7     | 7020  | 5845      | gi 50502        | collagen alpha chain precursor (AA -27 to 1127) [Mus musculus]  | 1       | 58     |
| 21     | 1   | 5     | 1     | 3234      | gi 1054860      | phosphoribosyl anthranilate isomerase [Thermotoga maritima]   | 1       | 58     |
| 23     | 1   | 2     | 1     | 2841      | gi 1276880      | [EpsG [Streptococcus thermophilus]  | 1       | 58     |
| 23     | 10  | 1     | 9301  | 8090      | pir A31133 A311 | diaminopimelate decarboxylase (EC 4.1.1.20) - Pseudomonas aeruginosa  | 1       | 58     |
| 38     | 129 | 1     | 22555 | 22884     | gi 973249       | vestitone reductase [Medicago sativa]   | 1       | 58     |
| 44     | 1   | 1     | 2     | 406       | gi 289272       | ferrichrome-binding protein [Bacillus subtilis]   | 1       | 58     |
| 45     | 1   | 1     | 1     | 552       | gi 29464        | embryonic myosin heavy chain (1085 AA) [Homo sapiens] ir S12460 S12460  | 1       | 58     |
| 55     | 1   | 2     | 759   | 538       | gi 158852       | glucose regulated protein [Echinococcus multilocularis]   | 1       | 58     |
| 62     | 13  | 1     | 8493  | 8068      | gi 975353       | kinase-associated protein B [Bacillus subtilis]   | 1       | 58     |
| 63     | 3   | 3     | 1553  | 1717      | gi 166926       | [Arabidopsis thaliana unidentified mRNA sequence, complete cds.], ene product [Arabidopsis thaliana]  | 1       | 58     |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop   | match           | match gene name   | % sim | % ident | length |
|--------|-----|--------|--------|-----------------|---|-------|---------|--------|
| ID     | ID  | (nt)   | (nt)   | accession       | (nt)  |       |         | (nt)   |
| 67     | 113 | 112017 | 11229  | gi 1228083      | NADH dehydrogenase subunit 2 [Chorthippus parallelus]                                       | 58    | 41      | 789    |
| 96     | 8   | 8208   | 9167   | gi 709992       | hypothesetical protein [Bacillus subtilis]  | 58    | 42      | 960    |
| 107    | 2   | 2065   | 1364   | gi 806327       | Escherichia coli hrpA gene for A protein similar to yeast PRP16 and RP22 [Escherichia coli] | 58    | 37      | 702    |
| 112    | 7   | 4519   | 5613   | gi 155588       | glucose-fructose oxidoreductase [Zymomonas mobilis] pir A42289 A42289                       | 58    | 38      | 1095   |
|        |     |        |        |                 | glucose-fructose oxidoreductase (EC 1.1.-.-) recursor - Zymomonas mobilis                   |       |         |        |
| 114    | 6   | 7318   | 6503   | gi 1377843      | unknown [Bacillus subtilis]   | 58    | 38      | 816    |
| 143    | 2   | 2261   | 1395   | pir A45605 A456 | immature-parasite-infected erythrocyte surface antigen MESA - Plasmodium falciparum         | 58    | 31      | 867    |
| 151    | 2   | 717    | 950    | gi 1370261      | unknown [Mycobacterium tuberculosis]  | 58    | 31      | 234    |
| 154    | 6   | 6015   | 4627   | gi 1209277      | pCTHom1 gene product [Chlamydia trachomatis]  | 58    | 41      | 1389   |
| 154    | 16  | 114281 | 113541 | gi 146613       | DNA ligase (EC 6.5.1.2) [Escherichia coli]  | 58    | 39      | 741    |
| 155    | 3   | 2269   | 1892   | gi 1303917      | YqIB [Bacillus subtilis]  | 58    | 34      | 378    |
| 174    | 1   | 1056   | 529    | gi 904198       | hypothesetical protein [Bacillus subtilis]  | 58    | 26      | 528    |
| 189    | 4   | 1533   | 1769   | gi 467383       | DNAbinding protein (probable) [Bacillus subtilis]   | 58    | 25      | 237    |
| 201    | 3   | 2669   | 3307   | gi 1511453      | endonuclease III [Methanococcus jannaschii]   | 58    | 34      | 639    |
| 208    | 1   | 1      | 238    | gi 1276729      | phycobilisome linker polypeptide [Porphyra purpurea]  | 58    | 29      | 237    |
| 220    | 111 | 14575  | 13058  | gi 397526       | clumping factor [Staphylococcus aureus]   | 58    | 51      | 1518   |
| 231    | 3   | 1629   | 1474   | gi 1002520      | MutS [Bacillus subtilis]  | 58    | 45      | 156    |
| 233    | 6   | 4201   | 3497   | gi 1463023      | [No definition line found [Caenorhabditis elegans]]   | 58    | 39      | 705    |
| 243    | 110 | 9303   | 110082 | gi 537207       | ORF_f277 [Escherichia coli]   | 58    | 32      | 780    |
| 257    | 1   | 331    | 1143   | gi 1340128      | ORF1 [Staphylococcus aureus]  | 58    | 44      | 813    |
| 302    | 2   | 460    | 801    | gi 40174        | ORF_X [Bacillus subtilis]   | 58    | 34      | 342    |
| 307    | 111 | 6984   | 6127   | gi 1303842      | YqfU [Bacillus subtilis]  | 58    | 30      | 858    |
| 321    | 3   | 1914   | 2747   | gi 1239996      | hypothesetical protein [Bacillus subtilis]  | 58    | 41      | 834    |
| 342    | 4   | 2724   | 3497   | gi 454838       | ORF_6; putative [Pseudomonas aeruginosa]  | 58    | 41      | 774    |
| 348    | 1   | 1      | 663    | gi 467478       | unknown [Bacillus subtilis]   | 58    | 36      | 663    |
| 401    | 2   | 384    | 605    | gi 143407       | para-aminobenzoic acid synthase, component I (pab) [Bacillus subtilis]                      | 58    | 53      | 222    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop | match          | match gene name  | % sim | % ident | length |
|--------|-----|-------|------|----------------|--|-------|---------|--------|
| ID     | ID  | (nt)  | (nt) | accession      | (nt)   |       |         | (nt)   |
| 437    | 1   | 325   | 1554 | gi 1303866     | YqgS [Bacillus subtilis]   | 58    | 35      | 1230   |
| 445    | 1   | 105   | 1442 | gi 581583      | protein A [Staphylococcus aureus]  | 58    | 32      | 1338   |
| 453    | 3   | 789   | 965  | gi 1009455     | unknown [Schizosaccharomyces pombe]  | 58    | 34      | 177    |
| 453    | 5   | 2748  | 2047 | gi 537214      | lyjG gene product [Escherichia coli]   | 58    | 40      | 702    |
| 479    | 2   | 731   | 1444 | gi 1256621     | 126.7% of identity in 165 aa to a Thermophilic bacterium hypothetical protein 6; putative [Bacillus subtilis]  | 58    | 36      | 714    |
| 490    | 1   | 909   | 547  | gi 580920      | lrodD (graA) polypeptide (AA 1-673) [Bacillus subtilis] pir S06048 [S06048]  | 58    | 36      | 363    |
|        |     |       |      |                | probable rodD protein - Bacillus subtilis sp P13484 TAGE_BACSU PROBABLE POLY(GLYCEROL-PHOSPHATE) LPHA-GLUCOSYLTRANSFERASE (EC 2.4.1.52) (TECHOIC ACID BIOSYNTHESIS PROTEIN E). |       |         |        |
| 517    | 1   | 1     | 1164 | sp P47264 Y018 | HYPOTHETICAL HELICASE MG018.   | 58    | 30      | 1164   |
| 517    | 6   | 4182  | 4544 | gi 453422      | orf268 gene product [Mycoplasma hominis]   | 58    | 29      | 363    |
| 546    | 3   | 2802  | 4019 | gi 886052      | restriction modification system S subunit [Spiroplasma citri] gi 886052  | 58    | 37      | 1218   |
|        |     |       |      |                | restriction modification system S subunit [Spiroplasma citri]  |       |         |        |
| 562    | 1   | 3     | 179  | gi 43831       | lnifS protein (AA 1-400) [Klebsiella pneumoniae]   | 58    | 34      | 177    |
| 600    | 2   | 1347  | 1156 | gi 1183819     | unknown [Pseudomonas aeruginosa]   | 58    | 48      | 192    |
| 604    | 2   | 1231  | 1001 | gi 1001353     | HYPOTHETICAL PROTEIN [Synchocystis sp.]  | 58    | 41      | 231    |
| 619    | 1   | 1     | 504  | gi 903748      | integral membrane protein [Homo sapiens]   | 58    | 43      | 504    |
| 625    | 1   | 2     | 364  | gi 1208474     | HYPOTHETICAL PROTEIN [Synchocystis sp.]  | 58    | 43      | 363    |
| 635    | 1   | 1492  | 755  | gi 1510995     | transaldolase [Methanococcus jannaschii]   | 58    | 41      | 738    |
| 645    | 1   | 1     | 846  | gi 677882      | lileal sodium-dependent bile acid transporter [Rattus norvegicus] gi 677882  | 58    | 33      | 846    |
|        |     |       |      |                | lileal sodium-dependent bile acid transporter [Rattus norvegicus]  |       |         |        |
| 645    | 3   | 906   | 1556 | gi 1239999     | HYPOTHETICAL PROTEIN [Bacillus subtilis]   | 58    | 41      | 651    |
| 665    | 1   | 771   | 532  | gi 1204262     | HYPOTHETICAL PROTEIN (GB L10328_61) [Haemophilus influenzae]   | 58    | 39      | 240    |
| 674    | 1   | 635   | 327  | gi 498817      | ORF8; homologous to small subunit of phage terminases [Bacillus subtilis]  | 58    | 39      | 309    |
| 675    | 2   | 1312  | 806  | gi 42181       | lsmC gene product [Escherichia coli]   | 58    | 28      | 507    |
| 745    | 1   | 618   | 310  | gi 120532      | coenzyme FQO synthesis protein III (pggIII) [Haemophilus influenzae]   | 58    | 32      | 309    |
| 799    | 2   | 242   | 1174 | gi 1204669     | collagenase [Haemophilus influenzae]   | 58    | 36      | 933    |
| 800    | 2   | 1096  | 614  | gi 171963      | tRNA isopentenyl transferase [Saccharomyces cerevisiae]  | 58    | 37      | 483    |
|        |     |       |      |                | sp P07804 MOD5 YEAST tRNA ISOPENTENYLTRANSFERASE (EC 2.5.1.8) ISOPENTENYL-DIPHOSPHATE: tRNA ISOPENTENYLTRANSFERASE (IPP TRANSFERASE) (IPP).                                    |       |         |        |

## S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop  | match      | match gene name   | % sim | % ident | length |
|--------|-----|--------|-------|------------|---|-------|---------|--------|
| ID     | ID  | (nt)   | (nt)  | accession  |   |       |         | (nt)   |
| 854    | 1   | 1108   | 605   | gi 466778  | lysine specific permease [Escherichia coli]   | 58    | 44      | 504    |
| 885    | 1   | 481    | 242   | gi 861199  | protochlorophyll IX Mg-chelatase subunit precursor [Hordeum vulgare]  | 58    | 33      | 240    |
| 891    | 1   | 3      | 527   | gi 1293660 | AbsA2 [Streptomyces coelicolor]   | 58    | 31      | 525    |
| 942    | 1   | 931    | 467   | gi 405567  | lrrAH [Plasmid pSK41]   | 58    | 30      | 465    |
| 1002   | 1   | 952    | 521   | gi 577649  | preLUM [Staphylococcus aureus]  | 58    | 34      | 432    |
| 1438   | 1   | 1      | 261   | gi 581558  | isoleucyl tRNA synthetase [Staphylococcus aureus] sp P41368 SYTP_STAAU<br>  ISOLEUCYL-TRNA SYNTHETASE, MUPirocin RESISTANT EC 6.1.1.5 (ISOLEUCINE--<br>  TRNA LIGASE) (ILERS) (MUPirocin RESISTANCE PROTEIN). | 58    | 30      | 261    |
| 1442   | 1   | 2      | 463   | gi 971394  | similar to Acc.No. D26185 [Escherichia coli]  | 58    | 34      | 462    |
| 1873   | 1   | 480    | 241   | gi 1339951 | small subunit of NADH-dependent glutamate synthase [Plectonema boryanum]  | 58    | 38      | 240    |
| 1876   | 1   | 3      | 158   | gi 529216  | No definition line found [Caenorhabditis elegans] sp P46503 YX7_CAEEL<br>  HYPOTHETICAL 7.3 KD PROTEIN F23F12.7 IN HROMOSOME III.   | 58    | 33      | 156    |
| 1989   | 1   | 108    | 401   | gi 1405458 | YneR [Bacillus subtilis]  | 58    | 29      | 294    |
| 2109   | 1   | 3      | 401   | gi 1001801 | hypothetical protein [Synechocystis sp.]  | 58    | 31      | 399    |
| 2473   | 1   | 288    | 145   | gi 510140  | Ligoendopeptidase F [Lactococcus lactis]  | 58    | 38      | 144    |
| 2523   | 1   | 452    | 228   | gi 644873  | catabolic dehydroquinate dehydratase [Acinetobacter calcoaceticus]  | 58    | 37      | 225    |
| 3041   | 1   | 2      | 211   | gi 1205367 | oligopeptide transport ATP-binding protein [Haemophilus influenzae]   | 58    | 39      | 210    |
| 3094   | 1   | 3      | 263   | gi 1185288 | isochorismate synthase [Bacillus subtilis]  | 58    | 38      | 261    |
| 3706   | 1   | 3      | 383   | gi 456614  | mevalonate kinase [Arabidopsis thaliana]  | 58    | 48      | 381    |
| 3854   | 1   | 1      | 402   | gi 808869  | human gcp372 [Homo sapiens]   | 58    | 32      | 402    |
| 4082   | 1   | 51     | 224   | gi 508551  | ribulose-1,5 bisphosphate carboxylase large subunit -methyltransferase<br>  [Pisum sativum]   | 58    | 37      | 174    |
| 4278   | 1   | 3      | 206   | gi 180189  | cerebellar-degeneration-related antigen (CD34) [Homo sapiens] gi 182737<br>  cerebellar degeneration-associated protein [Homo sapiens]<br>  pir A29770 A29770 cerebellar degeneration-related protein - human | 58    | 37      | 204    |
| 19     | 7   | 7818   | 7363  | gi 1001516 | hypothetical protein [Synechocystis sp.]  | 57    | 31      | 456    |
| 23     | 11  | 9663   | 8872  | gi 606066  | ORF_f256 [Escherichia coli]   | 57    | 29      | 792    |
| 31     | 1   | 4801   | 2402  | gi 153146  | ORF3 [Streptomyces coelicolor]  | 57    | 32      | 2400   |
| 38     | 14  | 11611  | 10796 | gi 144859  | ORF B [Clostridium perfringens]   | 57    | 31      | 816    |
| 46     | 14  | 112063 | 13046 | gi 1001319 | hypothetical protein [Synechocystis sp.]  | 57    | 25      | 984    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop | match            | match gene name  | % sim                       | % ident | length |      |
|--------|-----|-------|------|------------------|--|-----------------------------|---------|--------|------|
| ID     | ID  | (nt)  | (nt) | accession        |  |                             |         | (nt)   |      |
| 51     | 3   | 1411  | 1187 | lpir1B338561B338 | hypothetical 80K protein - <i>Bacillus sphaericus</i>                    | 57                          | 38      | 225    |      |
| 54     | 1   | 1     | 453  | lgi1684950       | staphylococcal accessory regulator A [Staphylococcus aureus]             | 57                          | 31      | 453    |      |
| 75     | 1   | 1     | 239  | lgi11000470      | [C27B7.7 [Caenorhabditis elegans]  | 57                          | 42      | 237    |      |
| 92     | 5   | 3855  | 3061 | lgi1143607       | sporulation protein [Bacillus subtilis]                                  | 57                          | 35      | 795    |      |
| 96     | 3   | 4006  | 4773 | lgi1144297       | lactyl esterase (XynC) [Caldocellum saccharolyticum] pir1B37202[B37202   | 57                          | 34      | 768    |      |
|        |     |       |      |                  | acetyl esterase (EC 3.1.1.6) (XynC) - <i>Caldoceillum accharolyticum</i> | 57                          | 1       | 1      |      |
| 107    | 1   | 3     | 1480 | 2076             | lgi1460955   | lTagE [Vibrio cholerae]     | 57      | 42     | 597  |
| 109    | 1   | 8     | 5340 | 5933             | lgi114388946   | Unknown [Bacillus subtilis] | 57      | 41     | 594  |
| 112    | 1   | 9     | 6679 | 7701             | lgi11486250  | Unknown [Bacillus subtilis] | 57      | 33     | 1023 |
| 114    | 4   | 6384  | 4108 | lgi1871456       | putative alpha subunit of formate dehydrogenase [Methanobacterium        | 57                          | 37      | 2277   |      |
| 126    | 2   | 430   | 1053 | lgi1288301       | [ORF2 gene product [Bacillus megaterium]                                 | 57                          | 37      | 624    |      |
| 131    | 5   | 6537  | 6277 | lgi11511160      | [M. jannaschii predicted coding region M11163 [Methanococcus jannaschii] | 57                          | 38      | 261    |      |
| 133    | 3   | 2668  | 2201 | lgi11303912      | [YqhW [Bacillus subtilis]  | 57                          | 40      | 468    |      |
| 133    | 4   | 3383  | 2784 | lgi11221884      | (urea?) amidolyase [Haemophilus influenzae]                              | 57                          | 37      | 600    |      |
| 147    | 4   | 2164  | 1694 | lgi1467469       | Unknown [Bacillus subtilis]  | 57                          | 33      | 471    |      |
| 160    | 2   | 1293  | 1060 | lgi1558604       | lchitin synthase 2 [Neurospora crassa]                                   | 57                          | 28      | 234    |      |
| 163    | 8   | 5687  | 4764 | lgi11455380      | lrrard gene product [Escherichia coli]                                   | 57                          | 38      | 924    |      |
| 168    | 6   | 4336  | 5325 | lgi139782        | 133kDa lipoprotein [Bacillus subtilis]                                   | 57                          | 32      | 990    |      |
| 170    | 5   | 3297  | 3455 | lgi1603404       | [Yer164p [Saccharomyces cerevisiae]                                      | 57                          | 37      | 159    |      |
| 221    | 6   | 8026  | 6809 | lgi11136221      | carboxypeptidase [Sulfolobus solfataricus]                               | 57                          | 32      | 1218   |      |
| 228    | 3   | 1348  | 1791 | lgi1288969       | lfbnecin binding protein [Streptococcus dysgalactiae] pir[S33850 S33850  | 57                          | 32      | 444    |      |
|        |     |       |      |                  | fibronectin-binding protein - <i>Streptococcus dysgalactiae</i>          | 57                          | 1       | 1      |      |
| 263    | 4   | 4411  | 3686 | lgi11185002      | ldihydrodipicolinate reductase [Pseudomonas syringae pv. tabaci]         | 57                          | 42      | 726    |      |
| 276    | 1   | 494   | 255  | lgi1396380       | [No definition line found [Escherichia coli]                             | 57                          | 40      | 240    |      |
| 283    | 2   | 335   | 1324 | lgi1773349       | BirA protein [Bacillus subtilis]   | 57                          | 32      | 990    |      |
| 297    | 1   | 469   | 236  | lgi11334820      | reading frame V [Cauliflower mosaic virus]                               | 57                          | 46      | 234    |      |
| 342    | 3   | 1993  | 2805 | lgi1120431       | hypothetical protein (SP:33644) [Haemophilus influenzae]                 | 57                          | 35      | 813    |      |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop | match            | match gene name  | % sim | % ident | length |
|--------|-----|-------|------|------------------|--|-------|---------|--------|
| ID     | ID  | (nt)  | (nt) | accession        |  | (nt)  | (nt)    | (nt)   |
| 375    | 6   | 3340  | 3741 | lgi 385177       | cell division protein [Bacillus subtilis]  | 57    | 26      | 402    |
| 433    | 6   | 3286  | 4011 | lgi 1524117      | alpha-acetolactate decarboxylase [Lactococcus lactis]  | 57    | 40      | 726    |
| 470    | 3   | 903   | 1145 | lgi 804819       | lprotein serine/threonine kinase [Toxoplasma gondii]   | 57    | 30      | 243    |
| 487    | 5   | 1391  | 1723 | lgi 507323       | lORF1 [Bacillus stearothermophilus]  | 57    | 28      | 333    |
| 498    | 1   | 274   | 852  | lgi 1334549      | lNADH-ubiquinone oxidoreductase subunit 4L [Podospora anserina]  | 57    | 34      | 579    |
| 503    | 1   | 343   | 173  | lgi 1502283      | lorganic cation transporter OCT2 [Rattus norvegicus]   | 57    | 30      | 171    |
| 505    | 2   | 1619  | 1284 | lgi 466884       | lB1496_C2_194 [Mycobacterium leprae]   | 57    | 40      | 336    |
| 519    | 2   | 1182  | 2549 | lgi 1303707      | lYrkH [Bacillus subtilis]  | 57    | 34      | 1368   |
| 522    | 2   | 3234  | 1945 | lgi 1064809      | lhomologous to sp:HTRA_ECOLI [Bacillus subtilis]   | 57    | 36      | 1290   |
| 538    | 2   | 909   | 1415 | lgi 153179       | lphosphorinothycin n-acetyltransferase [Streptomyces coelicolor]<br>lpir JH0246 JH0246 phosphinothricin N-acetyltransferase (EC 2.3.1.-)<br>lStreptomyces coelicolor | 57    | 40      | 507    |
| 547    | 1   | 968   | 486  | lgi 467340       | lunknown [Bacillus subtilis]   | 57    | 50      | 483    |
| 599    | 1   | 1062  | 532  | lsp P20692 TYRA_ | lPREPHENATE DEHYDROGENASE (EC 1.3.1.12) (PDH).   | 57    | 41      | 531    |
| 620    | 2   | 757   | 572  | lgi 1107894      | lunknown [Schizosaccharomyces pombe]   | 57    | 38      | 186    |
| 622    | 2   | 1600  | 1130 | lgi 173028       | lthioredoxin II [Saccharomyces cerevisiae]   | 57    | 39      | 471    |
| 625    | 2   | 362   | 1114 | lgi 1262366      | lhypothetical protein [Mycobacterium leprae]   | 57    | 34      | 753    |
| 680    | 1   | 1     | 204  | lgi 143544       | lRNA polymerase sigma-30 factor [Bacillus subtilis] pir A28625 A28625  | 57    | 30      | 204    |
| 696    | 1   | 2     | 433  | lgi 413972       | lipa-48r gene product [Bacillus subtilis]  | 57    | 33      | 432    |
| 704    | 1   | 36    | 638  | lgi 1499931      | M. jannaschii predicted coding region MJ1083 [Methanococcus jannaschii]  | 57    | 36      | 603    |
| 732    | 1   | 2316  | 1621 | lgi 1418959      | lorf4 [Lactobacillus sake]   | 57    | 37      | 696    |
| 746    | 1   | 451   | 227  | lgi 392973       | lRab3 [Aplysia californica]  | 57    | 42      | 225    |
| 757    | 1   | 20    | 466  | lgi 43979        | lL.curvatus small cryptic plasmid gene for rep protein [Lactobacillus<br>lrvatus]  | 57    | 45      | 447    |
| 862    | 1   | 2     | 295  | lgi 1303827      | lYqf1 [Bacillus subtilis]  | 57    | 21      | 294    |
| 1049   | 1   | 907   | 455  | lgi 1510108      | lORF-1 [Agrobacterium tumefaciens]   | 57    | 35      | 453    |
| 1117   | 1   | 1387  | 695  | lgi 896286       | lNH2 terminus uncertain [Leishmania tarentolae]  | 57    | 28      | 693    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

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|--------|------|-------|-------|-----------|-----------------|--|---------|--------|-----|
| ID     | ID   | (nt)  | (nt)  | accession |                 | (nt)   | (nt)    |        |     |
| 1      | 1136 | 1     | 2     | 322       | lgi 1303853     | YggF [Bacillus subtilis]   | 57      | 38     | 321 |
| 1      | 1144 | 2     | 1033  | 611       | lgi 310083      | voltage-activated calcium channel alpha-1 subunit [Rattus norvegicus]                                    | 57      | 46     | 423 |
| 1      | 1172 | 1     | 1472  | 738       | lgi 1511146     | [M. jannaschii] predicted coding region MJ11143 [Methanococcus jannaschii]                               | 57      | 28     | 735 |
| 1      | 1500 | 2     | 746   | 558       | lgi 142780      | putative membrane protein; putative [Bacillus subtilis]  | 57      | 35     | 189 |
| 1      | 1676 | 1     | 659   | 399       | lgi 313777      | luracil permease [Escherichia coli]  | 57      | 31     | 261 |
| 1      | 2481 | 1     | 2     | 400       | lgi 1237015     | lORF4 [Bacillus subtilis]  | 57      | 23     | 399 |
| 1      | 3099 | 1     | 3     | 230       | lgi 1204540     | lisochorismate synthase [Haemophilus influenzae]   | 57      | 39     | 228 |
| 1      | 3122 | 1     | 360   | 181       | lgi 882472      | lORF_0164 [Escherichia coli]   | 57      | 40     | 180 |
| 1      | 3560 | 1     | 2     | 361       | lgi 153490      | ltetraacycycin C resistance and export protein [Streptomyces laucaescens]                                | 57      | 37     | 360 |
| 1      | 3850 | 1     | 856   | 434       | lgi 155588      | lglucose-fructose oxidoreductase [Zymomonas mobilis] pir A42289 A42289                                   | 57      | 40     | 423 |
| 1      | 3931 | 1     | 704   | 354       | lgi 413953      | lipa-29d gene product [Bacillus subtilis]  | 57      | 36     | 351 |
| 1      | 3993 | 1     | 1     | 384       | lgi 151259      | [HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii] pir A44756 A44756                               | 57      | 39     | 384 |
| 1      | 4100 | 1     | 596   | 300       | lgi 1086633     | hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) Pseudomonas sp.  | 57      | —      | —   |
| 1      | 4065 | 1     | 793   | 398       | pir JY0037 RDEC | nitrate reductase (EC 1.7.99.4) alpha chain - Escherichia coli   | 57      | 31     | 396 |
| 1      | 4163 | 1     | 571   | 287       | lgi 21512       | HMG-CoA reductase (EC 1.1.1.88) [Solanum tuberosum]  | 57      | 50     | 285 |
| 1      | 4267 | 2     | 631   | 335       | lgi 1000365     | SpoIIAG [Bacillus subtilis]  | 57      | 38     | 297 |
| 1      | 4358 | 1     | 3     | 302       | lgi 298032      | EF [Streptococcus suis]  | 57      | 32     | 300 |
| 1      | 4389 | 2     | 108   | 290       | lgi 405894      | 1-phosphofructokinase [Escherichia coli]   | 57      | 37     | 183 |
| 1      | 4399 | 1     | 2     | 232       | lgi 1483603     | Pristinamycin I synthase I [Streptomyces pristinaespiralis]  | 57      | 35     | 231 |
| 1      | 4481 | 1     | 572   | 288       | lgi 405879      | lyeiR [Escherichia coli]   | 57      | 44     | 285 |
| 1      | 4486 | 1     | 512   | 258       | lgi 515938      | glutamate synthase (ferredoxin) [Synechocystis sp.] pir S46957 S46957                                    | 57      | 42     | 255 |
| 1      | 4510 | 1     | 481   | 242       | lgi 1205301     | glutamate synthase (ferredoxin) (EC 1.4.7.1) - ynechocystis  | 57      | 38     | 240 |
| 1      | 4617 | 1     | 468   | 256       | lgi 1511222     | leukotoxin secretion ATP-binding protein [Haemophilus influenzae]  | 57      | 35     | 213 |
| 1      | 4    | 11    | 12201 | 11524     | lgi 149204      | restriction modification enzyme, subunit M1 [Methanococcus jannaschii]                                   | 56      | 31     | 678 |
|        |      |       |       |           |                 | histidine utilization repressor G [Klebsiella aerogenes] pir A36730 A36730                               |         |        |     |
|        |      |       |       |           |                 | hurtG protein - Klebsiella pneumoniae (fragment) sp P19452 HUTG_KLEAE                                    |         |        |     |
|        |      |       |       |           |                 | FORMIMINOGLUTAMATE (EC 3.5.3.8) FORMIMINOGLUTAMATE HYDROLASE (HISTIDINE UTILIZATION PROTEIN G) FRAGMENT) |         |        |     |

## S. aureus - Putative coding regions of novel proteins similar to known proteins

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|--------|-----|--------|--------|------------|--|-------|---------|--------|
| ID     | ID  | (nt)   | (nt)   | accession  |  | (nt)  | (nt)    | (nt)   |
| 22     | 8   | 4248   | 5177   | gi 1322222 | [RACH1 [Homo sapiens]  | 56    | 33      | 930    |
| 38     | 128 | 121179 | 122264 | gi 1480705 | [lipote-protein ligase [Mycoplasma capricolum]                                     | 56    | 34      | 1086   |
| 44     | 3   | 1861   | 2421   | gi 490320  | [Y gene product [unidentified]   | 56    | 31      | 561    |
| 44     | 115 | 110103 | 10606  | gi 1205099 | [hypoetical protein (GB:Li19201_1) [Haemophilus influenzae]                        | 56    | 39      | 504    |
| 50     | 6   | 4820   | 5161   | gi 209931  | [fiber protein [Human adenovirus type 5]   | 56    | 48      | 342    |
| 53     | 4   | 2076   | 2972   | gi 623476  | [transcriptional activator [Providencia stuartii] sp P43463 [AARP_FROST]           | 56    | 30      | 897    |
| 67     | 6   | 5656   | 6594   | gi 466613  | [TRANSCRIPTIONAL ACTIVATOR AARP.   | 56    | 32      | 939    |
| 89     | 3   | 2364   | 1810   | gi 482922  | [protein with homology to pail repressor of B. subtilis [Lactobacillus elbrueckii] | 56    | 39      | 555    |
| 96     | 1   | 203    | 913    | gi 145594  | [cAMP receptor protein (crp) [Escherichia coli]                                    | 56    | 35      | 711    |
| 109    | 21  | 118250 | 17846  | gi 1204367 | [hypoetical protein (GB:U14003_278) [Haemophilus influenzae]                       | 56    | 27      | 405    |
| 112    | 8   | 5611   | 6678   | gi 155588  | [glucose-fructose oxidoreductase [Zymomonas mobilis] pir A42289 A42289             | 56    | 40      | 1068   |
| 131    | 3   | 6404   | 5100   | gi 619724  | [glucose-fructose oxidoreductase (EC 1.1.-.-) recursor - Zymomonas mobilis         | 56    | 30      | 1305   |
| 138    | 2   | 65     | 232    | gi 413918  | [MgtE [Bacillus firmus]  | 56    | 31      | 168    |
| 138    | 4   | 823    | 1521   | gi 580868  | [ipa-24d gene product [Bacillus subtilis]  | 56    | 31      | 699    |
| 146    | 2   | 740    | 447    | gi 1046009 | [M. genitalium predicted coding region MG309 [Mycoplasma genitalium]               | 56    | 37      | 294    |
| 149    | 2   | 1639   | 1067   | gi 945380  | [terminase small subunit [Bacteriophage LL-H]                                      | 56    | 35      | 573    |
| 163    | 1   | 2      | 223    | gi 143947  | [glutamine synthetase [Bacteroides fragilis]                                       | 56    | 30      | 222    |
| 166    | 5   | 6745   | 6449   | gi 405792  | [ORF154 [Pseudomonas putida]   | 56    | 26      | 297    |
| 187    | 1   | 31     | 393    | gi 311237  | [H (+)-transporting ATP synthase [Zea mays]  | 56    | 30      | 363    |
| 190    | 1   | 2      | 373    | gi 1109686 | [ProX [Bacillus subtilis]  | 56    | 35      | 372    |
| 191    | 8   | 11538  | 9943   | gi 581070  | [acyl coenzyme A synthetase [Escherichia coli]                                     | 56    | 35      | 1596   |
| 195    | 1   | 1291   | 647    | gi 1510242 | [collagenase [Methanococcus jannaschii]  | 56    | 34      | 645    |
| 230    | 3   | 2323   | 2072   | gi 40363   | [heat shock protein [Clostridium acetobutylicum]                                   | 56    | 39      | 252    |
| 238    | 5   | 3383   | 3775   | gi 1477533 | [sarA [Staphylococcus aureus]  | 56    | 31      | 393    |
| 270    | 2   | 813    | 1712   | gi 765073  | [autolysin [Staphylococcus aureus]   | 56    | 41      | 900    |

## S. aureus - Putative coding regions of novel proteins similar to known proteins

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|--------|-----|-------|------|-------------|---|-------|---------|--------|
| ID     | ID  | (nt)  | (nt) | accession   |   | (nt)  | (nt)    | (nt)   |
| 290    | 1   | 3221  | 1632 | gi 547513   | orf3 [Haemophilus influenzae]   | 1     | 56      | 34     |
| 297    | 5   | 1140  | 1373 | gi 1511556  | [M. jannaschii predicted coding region MJ1561 [Methanococcus jannaschii]                                      | 1     | 56      | 40     |
| 321    | 2   | 2947  | 1799 | gi 1001801  | hypothetical protein [Synechocystis sp.]  | 1     | 56      | 31     |
| 359    | 2   | 1279  | 641  | gi 46336    | [nolI gene product [Rhizobium meliloti]   | 1     | 56      | 26     |
| 371    | 2   | 360   | 1823 | gi 145304   | L-ribulokinase [Escherichia coli]   | 1     | 56      | 39     |
| 391    | 4   | 1762  | 2409 | gi 1001634  | [hypothetical protein [Synechocystis sp.]   | 1     | 56      | 34     |
| 402    | 1   | 380   | 192  | gi 1438904  | [5-HT4L receptor [Homo sapiens]   | 1     | 56      | 48     |
| 416    | 4   | 2480  | 2109 | gi 1408486  | [HS74A gene product [Bacillus subtilis]   | 1     | 56      | 31     |
| 424    | 3   | 1756  | 2334 | gi 142471   | lactolactate decarboxylase [Bacillus subtilis]  | 1     | 56      | 32     |
| 457    | 1   | 1907  | 1017 | gi 1205194  | [formamidopyrimidine-DNA glycosylase [Haemophilus influenzae]   | 1     | 56      | 36     |
| 458    | 2   | 2423  | 1812 | gi 15466    | [terminase [Bacteriophage SPP1]   | 1     | 56      | 37     |
| 504    | 2   | 2152  | 1283 | gi 1142681  | [Lpp38 [Pasteurella haemolytica]  | 1     | 56      | 38     |
| 511    | 1   | 1     | 1284 | gi 217049   | [brnQ protein [Salmonella typhimurium]  | 1     | 56      | 37     |
| 604    | 3   | 1099  | 1701 | gi 467109   | [rim; 30S Ribosomal protein S18 alanine acetyltransferase; 229 C1_170 [Mycobacterium leprae]                  | 1     | 56      | 43     |
| 660    | 5   | 3547  | 3774 | gi 1229106  | [ZK930.1 [Caenorhabditis elegans]   | 1     | 56      | 30     |
| 707    | 1   | 35    | 400  | gi 153929   | [NADPH-sulfite reductase flavoprotein component [Salmonella typhimurium]                                      | 1     | 56      | 38     |
| 709    | 2   | 1385  | 1095 | gi 1510801  | [hydrogenase accessory protein [Methanococcus jannaschii]   | 1     | 56      | 38     |
| 718    | 1   | 1     | 495  | gi 413948   | [lipa-24d gene product [Bacillus subtilis]  | 1     | 56      | 35     |
| 744    | 1   | 87    | 677  | gi 928836   | [repressor protein [Lactococcus lactis phage BK5-T]   | 1     | 56      | 35     |
| 790    | 1   | 776   | 399  | gi 1511513  | [ABC transporter, probable ATP-binding subunit [Methanococcus jannaschii]                                     | 1     | 56      | 33     |
| 795    | 1   | 1     | 3    | 407         | [gi 1205382 [cell division protein [Haemophilus influenzae]   | 1     | 56      | 34     |
| 813    | 1   | 19    | 930  | gi 1222161  | [permease [Haemophilus influenzae]  | 1     | 56      | 28     |
| 855    | 1   | 3     | 515  | gi 11256621 | [26.7% of identity in 165 aa to a Thermophilic bacterium hypothetical protein 6; putative [Bacillus subtilis] | 1     | 56      | 33     |
| 968    | 1   | 2     | 466  | gi 547513   | [orf3 [Haemophilus influenzae]  | 1     | 56      | 37     |
| 973    | 2   | 1049  | 732  | gi 886022   | [MexR [Pseudomonas aeruginosa]  | 1     | 56      | 31     |
| 1203   | 1   | 5     | 223  | gi 1184251  | [HMG-1 [Homo sapiens]   | 1     | 56      | 34     |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop  | match accession | match gene name  |
|--------|-----|--------|-------|-----------------|--|
| ID     | ID  | (nt)   | (nt)  |                 |  |
| 1976   | 1   | 452    | 237   | gi 9806         | lysine-rich aspartic acid-rich protein [Plasmodium chabaudi]<br>  r S22183 S22183 lysine/aspartic acid-rich protein - Plasmodium baudi |
| 2161   | 1   | 1      | 2     | 400             | gi 1237015   |
| 2958   | 1   | 1      | 362   | 183             | gi 466685  |
| 2979   | 1   | 1      | 421   | 212             | gi 1204354   |
| 2994   | 2   | 1      | 526   | 326             | gi 836646  |
| 3026   | 1   | 1      | 179   | 328             | gi 143306  |
| 3189   | 1   | 1      | 289   | 146             | gi 1166604   |
| 3770   | 1   | 1      | 63    | 401             | gi 1129145   |
| 4054   | 2   | 1      | 720   | 361             | gi 1205355   |
| 4145   | 1   | 1      | 1     | 324             | gi 1726095   |
| 4200   | 1   | 1      | 505   | 254             | gi 155588  |
| 4273   | 1   | 1      | 675   | 355             | gi 308861  |
| 1      | 1   | 3      | 4095  | 3436            | gi 5341  |
| 11     | 112 | 1      | 9377  | 8505            | gi 216773  |
| 12     | 4   | 5133   | 4534  | gi 467337       | haloacetate dehydrogenase H-1 [Moraxella sp.]  |
| 19     | 5   | 1      | 5404  | 5844            | gi 1001719   |
| 23     | 113 | 114087 | 12339 | gi 474190       | hypothetical protein [Synechocystis sp.]   |
| 32     | 1   | 7      | 5368  | 6888            | gi 1340096   |
| 34     | 3   | 1      | 2569  | 1808            | gi 1303968   |
| 34     | 5   | 1      | 3960  | 3412            | gi 1303962   |
| 36     | 1   | 1      | 1291  | 647             | gi 606045  |
| 36     | 6   | 1      | 6220  | 5243            | gi 1001341   |
| 47     | 3   | 1      | 3054  | 3821            | gi 1001819   |
| 49     | 1   | 1      | 2065  | 1127            | gi 403373  |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop  | match<br>accession | match<br>gene name  | % sim | % ident | length<br>(nt) |
|--------|-----|--------|-------|--------------------|---|-------|---------|----------------|
| ID     | ID  | (nt)   | (nt)  |                    |   |       |         |                |
| 67     | 111 | 8966   | 9565  | lgi 153053         | norA1199 protein [Staphylococcus aureus]                                      | 55    | 23      | 600            |
| 75     | 3   | 881    | 1273  | lgi 41698          | L-histidinol: NAD+ oxidoreductase (EC 1.1.1.23) (aa 1-434) [Escherichia coli] | 55    | 33      | 393            |
| 82     | 9   | 15387  | 14194 | lgi 1136221        | carboxypeptidase [Sulfolobus solfataricus]                                    | 55    | 35      | 1194           |
| 87     | 4   | 3517   | 4917  | lgi 1064812        | function unknown [Bacillus subtilis]  | 55    | 26      | 1401           |
| 88     | 2   | 1172   | 1636  | lgi 882463         | protein-N(pi)-phosphohistidine-sugar phosphotransferase [Escherichia coli]    | 55    | 35      | 465            |
| 92     | 1   | 127    | 516   | lgi 11377832       | function unknown [Bacillus subtilis]  | 55    | 36      | 390            |
| 100    | 2   | 836    | 2035  | lgi 1370274        | zeaxanthin epoxidase [Nicotiana plumbaginifolia]                              | 55    | 36      | 1200           |
| 100    | 5   | 5137   | 4658  | lgi 396660         | unknown open reading frame [Buchnera aphidicola]                              | 55    | 29      | 480            |
| 108    | 3   | 4266   | 2986  | lgi 1499866        | M. jannaschii predicted coding region MJ1024 [Methanococcus jannaschii]       | 55    | 31      | 1281           |
| 114    | 3   | 2616   | 1834  | lgi 1511367        | formate dehydrogenase, alpha subunit [Methanococcus jannaschii]               | 55    | 29      | 783            |
| 144    | 3   | 1805   | 1476  | lgi 1100787        | unknown [Saccharomyces cerevisiae]  | 55    | 35      | 330            |
| 165    | 5   | 6212   | 5508  | lgi 11045884       | M. genitalium predicted coding region MG199 [Mycoplasma genitalium]           | 55    | 27      | 705            |
| 189    | 5   | 2205   | 2576  | lgi 142569         | ATP synthase a subunit [Bacillus firmus]                                      | 55    | 35      | 372            |
| 191    | 6   | 9136   | 6857  | lgi 559411         | IB0272.3 [Caenorhabditis elegans]   | 55    | 34      | 273            |
| 194    | 2   | 364    | 636   | lgi 1145768        | IK7 kinesin-like protein [Dictyostelium discoideum]                           | 55    | 35      | 342            |
| 209    | 4   | 1335   | 1676  | lgi 473357         | ithi4 gene product [Schizosaccharomyces pombe]                                | 55    | 37      | 549            |
| 211    | 2   | 1693   | 1145  | lgi 1410130        | lORFX6 [Bacillus subtilis]  | 55    | 28      | 729            |
| 213    | 2   | 644    | 1372  | lgi 1633692        | lTrsA [Yersinia enterocolitica]   | 55    | 30      | 1338           |
| 214    | 7   | 4144   | 5481  | lgi 11001793       | hypothetical protein [Synchocystis sp.]                                       | 55    | 32      | 2277           |
| 221    | 7   | 111473 | 9197  | lgi 466520         | lpoCR [Salmonella typhimurium]  | 55    | 29      | 1506           |
| 233    | 8   | 5908   | 4817  | lgi 1237063        | lunkown [Mycobacterium tuberculosis]  | 55    | 38      | 1092           |
| 236    | 4   | 1375   | 2340  | lgi 1146199        | lputative [Bacillus subtilis]   | 55    | 32      | 966            |
| 243    | 2   | 380    | 1885  | lgi 459907         | lmercuric reductase [Plasmid p1258]   | 55    | 36      | 393            |
| 258    | 1   | 786    | 394   | lgi 455006         | lorf6 [Rhodococcus fascians]  | 55    | 35      | 813            |
| 281    | 1   | 126    | 938   | lgi 1408493        | homologous to SwissProt:YIDA_ECOLI hypothetical protein [Bacillus subtilis]   | 55    | 35      | 780            |
| 316    | 3   | 1323   | 2102  | lgi 1486447        | lLuxA homologue [Rhizobium sp.]   | 55    | 30      | 225            |
| 326    | 5   | 2968   | 2744  | lgi 1296824        | lproline iminopeptidase [Lactobacillus helveticus]                            | 55    | 36      | 225            |

| Contig | ORF | Start | Stop | match      | match gene name  | % sim | % ident | length |
|--------|-----|-------|------|------------|--|-------|---------|--------|
| ID     | ID  | (nt)  | (nt) | accession  |  | (nt)  | (nt)    |        |
| 351    | 2   | 2322  | 1429 | gi 1204820 | hydrogen peroxide-inducible activator [Haemophilus influenzae]   | 55    | 28      | 894    |
| 353    | 4   | 2197  | 2412 | gi 1272475 | lchitin synthase [Emericella nidulans]   | 55    | 50      | 216    |
| 380    | 1   | 14    | 379  | gi 142554  | ATP synthase i subunit [Bacillus megaterium]   | 55    | 37      | 366    |
| 383    | 1   | 462   | 232  | gi 289272  | ferrichrome-binding protein [Bacillus subtilis]  | 55    | 36      | 231    |
| 386    | 1   | 3     | 938  | gi 1510251 | DNase, putative [Methanococcus jannaschii]   | 55    | 30      | 936    |
| 410    | 2   | 1208  | 1891 | gi 1205144 | multidrug resistance protein [Haemophilus influenzae]  | 55    | 27      | 684    |
| 483    | 2   | 411   | 833  | gi 413934  | lipa-10r gene product [Bacillus subtilis]  | 55    | 26      | 423    |
| 529    | 3   | 1777  | 1433 | gi 606150  | ORF f309 [Escherichia coli]  | 55    | 33      | 345    |
| 555    | 1   | 1088  | 585  | gi 143407  | lpara-aminobenzoic acid synthase, component I (parB) [Bacillus subtilis]   | 55    | 28      | 504    |
| 565    | 1   | 402   | 202  | gi 1223961 | CDP-tyrolose epimerase [Yersinia pseudotuberculosis]   | 55    | 41      | 201    |
| 582    | 1   | 751   | 452  | gi 1256643 | 20.2% identity with NADH dehydrogenase of the Leishmania major<br>mitochondrion; putative [Bacillus subtilis]  | 55    | 36      | 300    |
| 645    | 5   | 2260  | 2057 | gi 210824  | fusion protein F [Bovine respiratory syncytial virus] pir JQ1481 VGNZBA<br>fusion glycoprotein precursor - bovine respiratory syncytial virus (strain<br>A51908) | 55    | 25      | 204    |
| 672    | 2   | 957   | 2216 | gi 1511333 | lM. jannaschii predicted coding region MJ1322 [Methanococcus jannaschii]   | 55    | 36      | 1260   |
| 730    | 1   | 955   | 479  | gi 537007  | ORF f379 [Escherichia coli]  | 55    | 30      | 477    |
| 737    | 1   | 1859  | 945  | gi 536963  | ICG Site No. 18166 [Escherichia coli]  | 55    | 30      | 915    |
| 742    | 2   | 228   | 572  | gi 304160  | product unknown [Bacillus subtilis]  | 55    | 38      | 345    |
| 817    | 2   | 1211  | 903  | gi 1136289 | histidine kinase A [Dictyostelium discoideum]  | 55    | 29      | 309    |
| 819    | 1   | 582   | 355  | gi 558073  | polymorphic antigen [Plasmodium falciparum]  | 55    | 22      | 228    |
| 832    | 2   | 1152  | 724  | gi 40367   | lORFC [Clostridium acetobutylicum]   | 55    | 32      | 429    |
| 840    | 1   | 769   | 386  | gi 1205875 | lpseudoouridylylate synthase I [Haemophilus influenzae]  | 55    | 39      | 384    |
| 1021   | 1   | 23    | 529  | gi 48563   | lbeta-lactamase [Yersinia enterocolitica]  | 55    | 38      | 507    |
| 1026   | 1   | 60    | 335  | gi 47804   | lOpp C (AA1-301) [Salmonella typhimurium]  | 55    | 26      | 276    |
| 1525   | 1   | 1     | 282  | gi 1477533 | lsarA [Staphylococcus aureus]  | 55    | 29      | 282    |
| 1814   | 2   | 224   | 985  | gi 1046078 | lM. genitalium predicted coding region MG369 [Mycoplasma genitalium]   | 55    | 38      | 762    |
| 3254   | 1   | 427   | 254  | gi 413968  | lipa-44d gene product [Bacillus subtilis]  | 55    | 30      | 174    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | ID   | Start  | Stop      | match      | match gene name  | % sim | % ident | length |
|--------|-----|------|--------|-----------|------------|--|-------|---------|--------|
| ID     | ID  | (nt) | (nt)   | accession |            |  |       |         | (nt)   |
| 3695   | 1   | 1    | 686    | 345       | gi 216773  | haloacetate dehalogenase H-1 [Moraxella sp.]                             | 55    | 32      | 342    |
| 3721   | 1   | 1    | 1      | 312       | gi 42029   | ORF1 gene product [Escherichia coli]                                     | 55    | 31      | 312    |
| 3799   | 1   | 1    | 3      | 272       | gi 42029   | ORF1 gene product [Escherichia coli]                                     | 55    | 38      | 270    |
| 3889   | 1   | 1    | 22     | 423       | gi 1129145 | lacyt1-CoA C-acyltransferase [Mangifera indica]                          | 55    | 45      | 402    |
| 3916   | 1   | 1    | 2      | 385       | gi 529754  | lspec [Streptococcus pyogenes]   | 55    | 38      | 384    |
| 3945   | 1   | 1    | 4      | 198       | gi 476252  | phase 1 flagellin [Salmonella enterica]                                  | 55    | 36      | 195    |
| 4074   | 1   | 1    | 488    | 246       | gi 42029   | ORF1 gene product [Escherichia coli]                                     | 55    | 38      | 243    |
| 4184   | 1   | 1    | 2      | 343       | gi 1524267 | lunkown [Mycobacterium tuberculosis]                                     | 55    | 28      | 342    |
| 4284   | 1   | 1    | 14     | 208       | gi 1100774 | ferredoxin-dependent glutamate synthase [Synechocystis sp.]              | 55    | 36      | 195    |
| 4457   | 2   | 1    | 644    | 378       | gi 180189  | cerebellar-degeneration-related antigen (CB34) [Homo sapiens]            | 55    | 38      | 267    |
|        |     |      |        |           |            | cerebellar degeneration-associated protein [Homo sapiens]                |       |         |        |
|        |     |      |        |           |            | pir A29770 A29770 cerebellar degeneration-related protein - human        |       |         |        |
| 4514   | 1   | 1    | 2      | 244       | gi 216773  | haloacetate dehalogenase H-1 [Moraxella sp.]                             | 55    | 32      | 243    |
| 4599   | 1   | 1    | 432    | 217       | gi 1129145 | lacyt1-CoA C-acyltransferase [Mangifera indica]                          | 55    | 42      | 216    |
| 4606   | 1   | 1    | 416    | 210       | gi 3886120 | lmyosin alpha heavy chain (S2 subfragment) (rabbits, masseter, ep tide   | 55    | 27      | 207    |
|        |     |      |        |           |            | Partial, 234 aa]   |       |         |        |
| 5      | 1   | 8    | 5348   | 4932      | gi 536069  | ORF YBL047c [Saccharomyces cerevisiae]                                   | 54    | 27      | 417    |
| 12     | 1   | 7    | 7166   | 6165      | gi 1205504 | homoserine acetyltransferase [Haemophilus influenzae]                    | 54    | 30      | 1002   |
| 23     | 1   | 16   | 117086 | 115326    | gi 474192  | liucc gene product [Escherichia coli]                                    | 54    | 31      | 1761   |
| 35     | 1   | 1    | 2      | 979       | gi 48054   | small subunit of soluble hydrogenase (AA 1-384) [Synechococcus sp.]      | 54    | 36      | 978    |
|        |     |      |        |           |            | iri S06919 HQYCSS soluble hydrogenase (EC 1.12.-.-) small chain -        |       |         |        |
|        |     |      |        |           |            | nechoococcus sp. (PCC 6716)  |       |         |        |
| 37     | 1   | 11   | 9437   | 8667      | gi 537207  | ORF f277 [Escherichia coli]  | 54    | 38      | 771    |
| 37     | 1   | 12   | 8165   | 8332      | gi 1160967 | palmitoyl-protein thioesterase [Homo sapiens]                            | 54    | 37      | 168    |
| 46     | 1   | 15   | 113025 | 113804    | gi 438473  | protein is hydrophobic, with homology to E. coli Prow; putative Bacillus | 54    | 28      | 780    |
|        |     |      |        |           |            | subtilis]  |       |         |        |
| 56     | 1   | 2    | 203    | 736       | gi 1256139 | YbbJ [Bacillus subtilis]   | 54    | 34      | 534    |
| 57     | 1   | 13   | 11117  | 10179     | gi 1151248 | inosine-uridine preferring nucleoside hydrolase [Crithidia fasciculata]  | 54    | 32      | 939    |
| 66     | 1   | 2    | 516    | 1133      | gi 1335781 | Cap [Drosophila melanogaster]  | 54    | 29      | 618    |
| 70     | 1   | 10   | 8116   | 8646      | gi 1399823 | PhoE [Rhizobium meliloti]  | 54    | 31      | 531    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop   | match            | match gene name  | % sim | % ident | length |
|--------|-----|--------|--------|------------------|--|-------|---------|--------|
| ID     | ID  | (nt)   | (nt)   | accession        |  | (nt)  |         |        |
| 70     | 115 | 12556  | 11801  | isp P02983 TCR_S | TETRACYCLINE RESISTANCE PROTEIN  | 54    | 29      | 756    |
| 87     | 5   | 4915   | 5706   | lgi 1064811      | function unknown [Bacillus subtilis]                                       | 54    | 33      | 792    |
| 92     | 4   | 3005   | 2289   | lgi 1205366      | oligopeptide transport ATP-binding protein [Haemophilus influenzae]        | 54    | 33      | 717    |
| 103    | 2   | 2596   | 1556   | lgi 1710495      | protein kinase [Bacillus brevis]   | 54    | 33      | 1041   |
| 105    | 2   | 3585   | 2095   | lgi 143727       | putative [Bacillus subtilis]   | 54    | 30      | 1491   |
| 112    | 4   | 2337   | 2732   | lgi 153724       | MalC [Streptococcus pneumoniae]  | 54    | 41      | 396    |
| 127    | 2   | 1720   | 2493   | lgi 144297       | lactyl esterase (XynC) [Caldocellum saccharolyticum] pir B37202 B37202     | 54    | 34      | 774    |
| 138    | 5   | 1600   | 3306   | lgi 142473       | lactylesterase (EC 3.1.1.6) (XynC) - Caldoccum accharolyticum              | 54    | 36      | 1707   |
| 152    | 2   | 525    | 1172   | lgi 1377834      | lunkown [Bacillus subtilis]  | 54    | 23      | 648    |
| 161    | 9   | 4831   | 5469   | lgi 903305       | lORF73 [Bacillus subtilis]   | 54    | 28      | 639    |
| 161    | 13  | 6694   | 7251   | lgi 1511039      | lphosphate transport system regulatory protein [Methanococcus jannaschii]  | 54    | 32      | 558    |
| 164    | 6   | 3263   | 4543   | lgi 1204976      | lprolyl-tRNA synthetase [Haemophilus influenzae]                           | 54    | 34      | 1281   |
| 164    | 120 | 121602 | 122243 | lgi 143582       | lspolIIIA protein [Bacillus subtilis]                                      | 54    | 32      | 642    |
| 171    | 6   | 5683   | 4250   | lgi 436965       | l[mlmA] gene products [Bacillus stearothermophilus] pir S43914 S43914      | 54    | 37      | 1434   |
| 206    | 18  | 119208 | 119720 | lgi 1240016      | lR09E10.3 [Caenorhabditis elegans]   | 54    | 38      | 513    |
| 218    | 2   | 1090   | 1905   | lgi 467378       | lunkown [Bacillus subtilis]  | 54    | 26      | 816    |
| 220    | 1   | 1322   | 663    | lgi 1353761      | lmyosin II heavy chain [Naegleria fowleri]                                 | 54    | 22      | 660    |
| 220    | 13  | 112655 | 113059 | pir S00485 S004  | l gene 11-1 protein precursor - Plasmodium falciparum (fragments)          | 54    | 35      | 405    |
| 221    | 3   | 2030   | 3709   | lgi 1303813      | lYqEW [Bacillus subtilis]  | 54    | 34      | 1680   |
| 272    | 7   | 5055   | 4219   | lgi 62964        | larylamine N-acetyltransferase (AA 1-290) [Gallus gallus] ir S06652 XYCHY3 | 54    | 33      | 837    |
| 316    | 7   | 4141   | 4701   | lgi 682769       | larylamine N-acetyltransferase (EC 2.3.1.5) (clone NAT-3) - chicken        | 54    | 31      | 561    |
| 316    | 110 | 6994   | 8742   | lgi 413951       | lipa-27d gene product [Bacillus subtilis]                                  | 54    | 28      | 1749   |
| 338    | 3   | 3377   | 2214   | lgi 490328       | lORF F [unidentified]  | 54    | 28      | 1164   |
| 341    | 4   | 3201   | 3614   | lgi 1171959      | lmyosin-like protein [Saccharomyces cerevisiae]                            | 54    | 25      | 414    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop | match  | match gene name  | % sim | % ident | length |
|--------|-----|-------|------|--|--|-------|---------|--------|
| ID     | ID  | (nt)  | (nt) | accession  |  | (nt)  | (nt)    | (nt)   |
| 346    | 1   | 1820  | 912  | gi 396400  | similar to eukaryotic Na <sup>+</sup> /H <sup>+</sup> exchangers [Escherichia coli]<br>sp P32703 YJCE_ECOLI HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS NTERGENIC<br>REGION (0549). | 54    | 34      | 909    |
| 348    | 2   | 623   | 1351 | gi 537109  | ORF f343a [Escherichia coli]   | 54    | 34      | 729    |
| 378    | 2   | 1007  | 1942 | sp P02983 TCR_S_I TETRACYCLINE RESISTANCE PROTEIN. |  | 54    | 31      | 936    |
| 408    | 6   | 4351  | 5301 | gi 474190  | liuCA gene product [Escherichia coli]  | 54    | 29      | 951    |
| 444    | 9   | 7934  | 8854 | gi 216267  | ORF2 [Bacillus megaterium]   | 54    | 32      | 921    |
| 463    | 2   | 2717  | 2229 | gi 304160  | product unknown [Bacillus subtilis]  | 54    | 50      | 489    |
| 502    | 2   | 1696  | 1133 | gi 1205015   | hypothetical protein (SP:PI0120) [Haemophilus influenzae]  | 54    | 38      | 564    |
| 505    | 6   | 6262  | 5357 | gi 1500558   | 12-hydroxyhepta-2,4-diene-1,7-dioate isomerase [Methanococcus jannaschii]  | 54    | 41      | 906    |
| 550    | 1   | 2736  | 1522 | gi 40100   | lrodC (tag3) polypeptide (AA 1-746) [Bacillus subtilis] ir S06049 S06049<br>lrodC protein - Bacillus subtilis p P13485 TAGF_BACSU TECHOIC ACID<br>BIOSYNTHESIS PROTEIN F.        | 54    | 35      | 1215   |
| 551    | 5   | 3305  | 4279 | gi 950197  | lunknow [Corynebacterium glutamicum]   | 54    | 34      | 975    |
| 558    | 2   | 1356  | 958  | gi 485090  | [No definition line found [Caenorhabditis elegans]   | 54    | 32      | 399    |
| 580    | 1   | 91    | 936  | gi 331906  | fused envelope glycoprotein precursor [Friend spleen focus-forming virus]  | 54    | 45      | 846    |
| 603    | 3   | 554   | 757  | gi 1323423   | lORF YGR234w [Saccharomyces cerevisiae]  | 54    | 36      | 204    |
| 617    | 1   | 25    | 249  | gi 219959  | ornithine transcarbamylase [Homo sapiens]  | 54    | 40      | 225    |
| 622    | 3   | 1097  | 1480 | gi 1303873   | YggZ [Bacillus subtilis]   | 54    | 25      | 384    |
| 623    | 1   | 3     | 404  | gi 1063250   | low homology to P20 protein of Bacillus licheniformis and bleomycin<br>acetyltransferase of Streptomyces verticillus [Bacillus subtilis]   | 54    | 45      | 402    |
| 689    | 1   | 1547  | 1011 | gi 552446  | [NADH dehydrogenase subunit 4 [Apis mellifera ligustica] pir S52968 S52968<br>  NADH dehydrogenase chain 4 - honeybee itochondrion (SGC4)  | 54    | 30      | 537    |
| 725    | 2   | 686   | 1441 | gi 987096  | l sensory protein kinase [Streptomyces hygroscopicus]  | 54    | 26      | 756    |
| 956    | 1   | 1     | 249  | pir S30782 S307                                    | l integrin homolog - yeast (Saccharomyces cerevisiae)  | 54    | 24      | 249    |
| 978    | 2   | 1137  | 859  | gi 1301994   | l ORF YNL091w [Saccharomyces cerevisiae]   | 54    | 33      | 279    |
| 1314   | 1   | 3     | 281  | gi 1001108   | l hypothetical protein [Synchocystis sp.]  | 4     | 33      | 279    |
| 2450   | 1   | 1     | 228  | gi 1045057   | l ch-TOG [Homo sapiens]  | 54    | 32      | 228    |
| 2934   | 1   | 1     | 387  | gi 580870  | l ipa-37d qoxA gene product [Bacillus subtilis]  | 54    | 36      | 387    |
| 2970   | 1   | 499   | 251  | sp P37348 YECE_I                                   | HYPOTHETICAL PROTEIN IN ASPS' REGION (FRAGMENT).   | 54    | 42      | 249    |

## S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop   | match<br>accession | match<br>gene name   | % sim | % ident | length<br>(nt) |
|--------|-----|--------|--------|--------------------|--|-------|---------|----------------|
| ID     | ID  | (nt)   | (nt)   |                    |  |       |         |                |
| 3002   | 1   | 1      | 309    | lgi 44027          | Tma protein [Lactococcus lactis]   | 54    | 33      | 309            |
| 3561   | 1   | 9      | 464    | lgi 151259         | [HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii] pir A44756 A44756<br>hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) Pseudomonas sp.  | 54    | 35      | 456            |
| 3572   | 1   | 72     | 401    | lgi 450688         | [hsdM gene of Ecoprr1 gene product [Escherichia coli] pir S38437 S38437 hsdM<br>protein - Escherichia coli pir S09629 S09629 hypothetical protein A -<br>Escherichia coli [SUB 40-520] | 54    | 36      | 330            |
| 3829   | 1   | 798    | 400    | lgi 1322245        | [mevalonate pyrophosphate decarboxylase [Rattus norvegicus]  | 54    | 29      | 399            |
| 3909   | 1   | 1      | 273    | lgi 29865          | [CENP-E [Homo sapiens]   | 54    | 30      | 273            |
| 3921   | 1   | 3      | 209    | pir S24325 S243    | [glucan 1,4-beta-glucosidase (EC 3.2.1.74) - Pseudomonas fluorescens subsp.<br>cellulosa   | 54    | 34      | 207            |
| 4438   | 1   | 566    | 285    | lgi 1196657        | [unknown protein [Mycoplasma pneumoniae]   | 54    | 30      | 282            |
| 4459   | 1   | 3      | 272    | lgi 1046081        | [hypothetical protein (GB:D26185_10) [Mycoplasma genitalium]   | 54    | 38      | 270            |
| 4564   | 1   | 3      | 221    | lgi 216267         | [ORF2 [Bacillus megaterium]  | 54    | 38      | 219            |
| 23     | 112 | 112538 | 110685 | lgi 474192         | [iucC gene product [Escherichia coli]  | 53    | 35      | 1854           |
| 23     | 114 | 114841 | 113579 | lgi 42029          | [ORF1 gene product [Escherichia coli]  | 53    | 32      | 1263           |
| 24     | 3   | 4440   | 3940   | lgi 1369947        | [c2 gene product [Bacteriophage B1]  | 53    | 36      | 501            |
| 26     | 4   | 3818   | 4618   | lgi 1486247        | [unknown [Bacillus subtilis]   | 53    | 37      | 801            |
| 38     | 6   | 2856   | 3998   | lgi 4058880        | [yeiI [Escherichia coli]   | 53    | 40      | 1143           |
| 38     | 110 | 9380   | 7806   | lgi 1399954        | [thyroid sodium/iodide symporter NIS [Rattus norvegicus]   | 53    | 29      | 1575           |
| 56     | 110 | 112324 | 121100 | pir A54592 A545    | [110k actin filament-associated protein - chicken  | 53    | 32      | 225            |
| 57     | 6   | 5047   | 4583   | pir A00341 DEZP    | [alcohol dehydrogenase (EC 1.1.1.1) - fission yeast (Schizosaccharomyces<br>pombe)   | 53    | 39      | 465            |
| 57     | 112 | 110515 | 8932   | lgi 1480429        | [putative transcriptional regulator [Bacillus stearothermophilus]  | 53    | 30      | 1584           |
| 67     | 112 | 9496   | 10218  | lgi 1511555        | [quinolone resistance nora protein [Methanococcus jannaschii]  | 53    | 31      | 723            |
| 69     | 3   | 3125   | 2382   | lgi 1087017        | [arabinogalactan-protein, AGP [Nicotiana alata, cell-suspension culture<br>filtrate, Peptide, 461 aa]  | 53    | 30      | 744            |
| 79     | 1   | 3      | 1031   | lgi 1523802        | [glucanase [Anabaena variabilis]   | 53    | 32      | 1029           |
| 80     | 1   | 673    | 338    | lgi 452428         | [ATPase 3 [Plasmodium falciparum]  | 53    | 36      | 336            |
| 88     | 4   | 1910   | 2524   | lgi 537034         | [ORF_0488 [Escherichia coli]   | 53    | 25      | 615            |
| 88     | 5   | 2467   | 3282   | lgi 537034         | [ORF_0488 [Escherichia coli]   | 53    | 29      | 816            |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop   | match           | gene name   | % sim | % ident | length |
|--------|-----|--------|--------|-----------------|---|-------|---------|--------|
| ID     | ID  | (nt)   | (nt)   | accession       |   |       |         | (nt)   |
| 92     | 8   | 5870   | 5505   | gi 399598       | lambphotropic murine retrovirus receptor [Rattus norvegicus]  | 53    | 33      | 366    |
| 94     | 5   | 4417   | 3239   | gi 173038       | ltryptomyosin (TPM1) [Saccharomyces cerevisiae]   | 53    | 25      | 1179   |
| 99     | 5   | 4207   | 5433   | sp P28246 BCR_E | BICYCLOMYCIN RESISTANCE PROTEIN (SULFONAMIDE RESISTANCE PROTEIN).   | 53    | 30      | 1227   |
| 120    | 3   | 1639   | 2262   | gi 576655       | ORF1 [Vibrio anguillarum]   | 53    | 35      | 624    |
| 120    | 111 | 7257   | 8897   | gi 1524397      | glycine betaine transporter OpUD [Bacillus subtilis]  | 53    | 33      | 1641   |
| 127    | 6   | 6893   | 5685   | gi 12566630     | putative [Bacillus subtilis]  | 53    | 32      | 1209   |
| 147    | 2   | 255    | 557    | gi 581648       | lepiB gene product [Staphylococcus epidermidis]   | 53    | 34      | 303    |
| 158    | 4   | 4705   | 4256   | gi 151004       | lmucoidy regulatory protein AlQR [Pseudomonas aeruginosa] pir A32002 A32802   | 53    | 32      | 450    |
|        |     |        |        |                 | regulatory protein alQR - Pseudomonas aeruginosa sp P26275 ALQR_PSEAE   |       |         |        |
|        |     |        |        |                 | POSITIVE ALGINATE BIOSYNTHESIS REGULATORY PROTEIN.  |       |         |        |
| 171    | 7   | 5717   | 5421   | gi 1510669      | hypothetical protein (GP:D6404_18) [Methanococcus jannaschii]   | 53    | 34      | 297    |
| 191    | 9   | 113087 | 11483  | gi 298085       | lactoacetate decarboxylase [Clostridium acetobutylicum] pir B4936 B49346  | 53    | 31      | 1605   |
|        |     |        |        |                 | butyrate-acetoacetate CoA-transferase (EC .8.3.9) small chain -   |       |         |        |
|        |     |        |        |                 | Clostridium acetobutylicum sp P33752 CTFA_CLOAB BUTYRATE-ACETOACETATE COA-TRANSFERASE SUBUNIT (EC 2.8.3.9) (COAT A) |       |         |        |
| 203    | 5   | 3763   | 4326   | gi 143456       | rpoe protein (ttg start codon) [Bacillus subtilis]  | 53    | 29      | 564    |
| 206    | 117 | 118204 | 118971 | gi 304136       | acetylglutamate kinase [Bacillus stearothermophilus] sp Q07905 ARGB_BACST   | 53    | 36      | 768    |
|        |     |        |        |                 | ACETYLGLUTAMATE KINASE (EC 2.7.2.8) (NAG INASE) (AGK) (N-ACETYL-L-GLUTAMATE 5-PHOSPHOTRANSFERASE).                  |       |         |        |
| 212    | 10  | 4021   | 4221   | gi 9878         | protein kinase [Plasmodium falciparum]  | 53    | 28      | 201    |
| 231    | 2   | 1580   | 1350   | gi 537506       | paramyosin [Dirofilaria immitis]  | 53    | 34      | 231    |
| 272    | 6   | 2719   | 3249   | pir A33141 A331 | hypothetical protein (gtfd 3' region) - Streptococcus mutans  | 53    | 34      | 531    |
| 308    | 3   | 927    | 2576   | gi 606292       | ORF_0696 (Escherichia coli)   | 53    | 33      | 1650   |
| 320    | 7   | 5645   | 5884   | gi 160596       | tRNA polymerase III largest subunit [Plasmodium falciparum]   | 53    | 33      | 240    |
|        |     |        |        |                 | sp P27625 RPC1_PLAFA DNA-DIRECTED RNA POLYMERASE III LARGEST UBNUNIT (EC 2.7.7.6).                                  |       |         |        |
| 327    | 1   | 218    | 901    | gi 1854601      | lunkown [Schizosaccharomyces pombe]   | 53    | 31      | 684    |
| 341    | 2   | 212    | 2500   | gi 633732       | ORF1 [Campylobacter jejuni]   | 53    | 31      | 2289   |
| 351    | 1   | 763    | 383    | sp P31675 YABM  | HYPOTHETICAL 42.7 KD PROTEIN IN TBPA-LEUD INTERGENIC REGION (ORF04).  | 53    | 32      | 381    |
| 433    | 7   | 5087   | 4731   | gi 1001961      | IMHC class II analog [Staphylococcus aureus]  | 53    | 30      | 357    |
| 454    | 2   | 1240   | 980    | pir A60328 A603 | 40K cell wall protein precursor (sr 5' region) - Streptococcus mutans   | 53    | 27      | 261    |
|        |     |        |        |                 | (strain OMZ175, serotype f)   |       |         |        |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop | match      | match gene name   | % sim | % ident | length |
|--------|-----|-------|------|------------|---|-------|---------|--------|
| ID     | ID  | (nt)  | (nt) | accession  |   | (nt)  | (nt)    | (nt)   |
| 470    | 4   | 1123  | 1761 | gi 516826  | rat GCP360 [Rattus rattus]  | 53    | 30      | 639    |
| 483    | 1   | 432   | 217  | gi 1480429 | putative transcriptional regulator [Bacillus stearothermophilus]  | 53    | 33      | 216    |
| 544    | 1   | 516   | 1259 | gi 46587   | ORF 1 (AA 1 - 121) (1 is 2nd base in codon) [Staphylococcus aureus]<br>ir S15765 S15765 hypothetical protein 1 (hlb 5' region) - aphylococcus   | 53    | 38      | 744    |
| 558    | 10  | 3957  | 3754 | gi 15140   | aureus (fragment)   | 53    | 32      | 204    |
| 603    | 2   | 339   | 620  | gi 507738  | Ires gene [Bacteriophage P1]<br>Hmp [Vibrio parahaemolyticus]   | 53    | 26      | 282    |
| 693    | 1   | 1669  | 941  | gi 153123  | toxic shock syndrome toxin-1 precursor [Staphylococcus aureus]<br>pir A24606 XC5AS1 toxic shock syndrome toxin-1 precursor - taphylococcus  | 53    | 38      | 729    |
| 766    | 1   | 2     | 673  | gi 687600  | orfA2; orfA2 forms an operon with orfA1 [Listeria monocytogenes]  | 53    | 43      | 672    |
| 781    | 1   | 667   | 335  | gi 1204551 | lpilin biogenesis protein [Haemophilus influenzae]  | 53    | 26      | 333    |
| 801    | 1   | 3     | 545  | gi 1279400 | lSapA protein [Escherichia coli]  | 53    | 25      | 543    |
| 803    | 1   | 2     | 910  | gi 695278  | lipase-like enzyme [Alcaligenes eutrophus]  | 53    | 30      | 909    |
| 872    | 1   | 1177  | 590  | gi 298032  | IEF [Streptococcus suis]  | 53    | 30      | 588    |
| 910    | 1   | 2     | 184  | gi 1044936 | unknown [Schizosaccharomyces pombe]   | 53    | 29      | 183    |
| 943    | 1   | 794   | 399  | gi 290508  | similar to unidentified ORF near 47 minutes [Escherichia coli]<br>sp P31436 YICK_ECOLI HYPOTHETICAL 43.5 KD PROTEIN IN SELC-NLPA_NTERGENIC  | 53    | 30      | 396    |
| 988    | 1   | 1004  | 504  | gi 142441  | ORF 3; putative [Bacillus subtilis]   | 53    | 28      | 501    |
| 1064   | 1   | 3     | 434  | gi 305080  | lmyosin heavy chain [Entamoeba histolytica]   | 53    | 26      | 432    |
| 1366   | 1   | 3     | 452  | gi 308852  | transmembrane protein [Lactococcus lactis]  | 53    | 33      | 450    |
| 1758   | 1   | 792   | 397  | gi 1001774 | hypothetical protein [Synechocystis sp.]  | 53    | 30      | 396    |
| 1897   | 1   | 1     | 447  | gi 1303949 | YqIX [Bacillus subtilis]  | 53    | 27      | 447    |
| 2381   | 1   | 798   | 400  | gi 1146243 | 22.4% identity with Escherichia coli DNA-damage inducible protein ...;<br>putative [Bacillus subtilis]  | 53    | 37      | 399    |
| 3537   | 1   | 1     | 327  | gi 450688  | hsdM gene of Ecoprr1 gene product [Escherichia coli] pir S38437 S38437 hsdM<br>protein - Escherichia coli pir S09629 S09629 hypothetical protein A -<br>Escherichia coli (SUB 40-520) | 53    | 35      | 327    |
| 3747   | 2   | 137   | 397  | gi 1477486 | transposase [Burkholderia cepacia]  | 53    | 53      | 261    |
| 11     | 5   | 3049  | 3441 | gi 868224  | No definition line found [Caenorhabditis elegans]   | 52    | 33      | 393    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop   | match        | match gene name | % sim       | % ident     | length |
|--------|-----|--------|--------|--------------|-----------------|-------------|-------------|--------|
| ID     | ID  | (nt)   | (nt)   | accession    |                 | (nt)        | (nt)        | (nt)   |
| 15     | 5   | 2205   | 2369   | lgi 215966   | lgi 1205379     | lgi 1205379 | lgi 1205379 | 165    |
| 19     | 3   | 2429   | 3808   | lgi 579124   | lgi 1205379     | lgi 1205379 | lgi 1205379 | 1380   |
| 24     | 1   | 6920   | 3462   | lgi 1205379  | lgi 1205379     | lgi 1205379 | lgi 1205379 | 3459   |
| 37     | 5   | 3015   | 3935   | lgi 1500543  | lgi 1205379     | lgi 1205379 | lgi 1205379 | 921    |
| 38     | 13  | 8795   | 9703   | lgi 46851    | lgi 1205379     | lgi 1205379 | lgi 1205379 | 909    |
| 44     | 16  | 110617 | 111066 | lgi 42012    | lgi 1205379     | lgi 1205379 | lgi 1205379 | 450    |
| 46     | 1   | 3      | 521    | lgi 1040957  | lgi 1205379     | lgi 1205379 | lgi 1205379 | 519    |
| 51     | 10  | 5531   | 6280   | lgi 388269   | lgi 1205379     | lgi 1205379 | lgi 1205379 | 750    |
| 56     | 5   | 3968   | 2826   | lgi 181949   | lgi 1205379     | lgi 1205379 | lgi 1205379 | 1143   |
| 57     | 5   | 4850   | 4173   | lgi 304153   | lgi 1205379     | lgi 1205379 | lgi 1205379 | 678    |
| 62     | 5   | 3364   | 2870   | lgi 11072399 | lgi 1205379     | lgi 1205379 | lgi 1205379 | 495    |
| 62     | 6   | 4445   | 3651   | lgi 46485    | lgi 1205379     | lgi 1205379 | lgi 1205379 | 795    |
| 67     | 14  | 111355 | 12962  | lgi 1511365  | lgi 1205379     | lgi 1205379 | lgi 1205379 | 1608   |
| 67     | 21  | 116935 | 18158  | lgi 1204393  | lgi 1205379     | lgi 1205379 | lgi 1205379 | 1224   |
| 70     | 4   | 2185   | 1997   | lgi 17227    | lgi 1205379     | lgi 1205379 | lgi 1205379 | 189    |
| 96     | 10  | 110005 | 10664  | lgi 11408485 | lgi 1205379     | lgi 1205379 | lgi 1205379 | 660    |
| 103    | 5   | 3986   | 3351   | lgi 1009368  | lgi 1205379     | lgi 1205379 | lgi 1205379 | 636    |
| 109    | 3   | 4102   | 3350   | lgi 699274   | lgi 1205379     | lgi 1205379 | lgi 1205379 | 753    |
| 109    | 19  | 115732 | 17300  | lgi 1526981  | lgi 1205379     | lgi 1205379 | lgi 1205379 | 1569   |
| 121    | 3   | 1412   | 981    | lgi 1732931  | lgi 1205379     | lgi 1205379 | lgi 1205379 | 432    |
| 125    | 3   | 865    | 1680   | lgi 11296975 | lgi 1205379     | lgi 1205379 | lgi 1205379 | 816    |
| 130    | 2   | 659    | 1807   | lgi 1256634  | lgi 1205379     | lgi 1205379 | lgi 1205379 | 1149   |
| 149    | 1   | 1164   | 583    | lgi 1225943  | lgi 1205379     | lgi 1205379 | lgi 1205379 | 582    |
| 149    | 14  | 4687   | 4415   | lgi 1510368  | lgi 1205379     | lgi 1205379 | lgi 1205379 | 273    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop | match     | gene name   |
|--------|-----|-------|------|-----------|---|
| ID     | ID  | (nt)  | (nt) | accession |   |
| 1      | 167 | 1     | 216  | 1001      | gi 146025  cell division protein [Escherichia coli]   |
| 188    | 1   | 1     | 120  | 1256      | gi 474915  orf 337; translated orf of similarity to SW: BCR_ECOLI_bicyclomycin_resistance   |
|        |     |       |      |           | protein of Escherichia coli [Coxiella burnetii] Pir S44207  hypothetical protein 337 - Coxiella burnetii (SUB -338)   |
| 195    | 9   | 9     | 9161 | 8760      | gi 3028  mitochondrial outer membrane 72K protein [Neurospora crassa]  r A36682 A36682 72K mitochondrial outer membrane protein - rospora crassa  |
| 200    | 1   | 3     | 2065 | 2607      | gi 142439  ATP-dependent nuclease [Bacillus subtilis]   |
| 203    | 4   | 4     | 2776 | 3684      | gi 1303698  BltD [Bacillus subtilis]  |
| 227    | 8   | 8     | 5250 | 5651      | gi 305080  Imyosin heavy chain [Entamoeba histolytica]  |
| 242    | 1   | 1     | 21   | 1424      | gi 1060877  EmrY [Escherichia coli]   |
| 249    | 5   | 5     | 4526 | 4753      | pir C37222 C372  cytochrome P450 1A1, hepatic - dog (fragment)  |
| 255    | 1   | 1     | 2107 | 1055      | gi 143290  penicillin-binding protein [Bacillus subtilis]   |
| 276    | 7   | 7     | 3963 | 3664      | gi 1001610  hypothetical protein [Synechocystis sp.]  |
| 276    | 8   | 8     | 4456 | 4055      | gi 416235  orf L3 [Mycoplasma capricolum]   |
| 289    | 1   | 2     | 1856 | 1449      | gi 150900  GTP phosphohydrolase [Proteus vulgaris]  |
| 325    | 1   | 1     | 1    | 279       | gi 1204874  polypeptide deformylase (formylmethionine deformylase) [Haemophilus influenzae]   |
| 340    | 1   | 1     | 2017 | 1010      | gi 1215695  peptide transport system protein SapE homolog; SapF homolog [Mycoplasma pneumoniae]   |
| 375    | 3   | 3     | 340  | 1878      | gi 1467446  similar to SpovB [Bacillus subtilis]  |
| 424    | 4   | 4     | 4104 | 3262      | gi 1478239  unknown [Mycobacterium tuberculosis]  |
| 430    | 1   | 1     | 3    | 575       | pir A42606 A426  orfA 5' to orf405 - Saccharopolyspora erythraea (fragment)   |
| 444    | 4   | 4     | 4728 | 3712      | gi 1408494  homologous to penicillin acylase [Bacillus subtilis]  |
| 465    | 1   | 1     | 1802 | 903       | gi 143331  alkaline phosphatase regulatory protein [Bacillus subtilis]  pir A27650 A27650 regulatory protein phoR - Bacillus subtilis  sp P23515 PHOR_BACSU_ALKALINE_PHOSPHATASE_SYNTHESIS_SENSOR_PROTEIN_HOR (EC 2.7.3.-). |
| 469    | 5   | 5     | 4705 | 4169      | gi 755152  highly hydrophobic integral membrane protein [Bacillus subtilis]  sp P42953 TAGBACSU_TEICHOIC_ACID_TRANSLOCATION_PERMEASE_PROTEIN_4GG.   |
| 495    | 1   | 1     | 1262 | 633       | gi 1204607  transcription activator [Haemophilus influenzae]  |
| 505    | 7   | 7     | 6004 | 5762      | gi 142440  ATP-dependent nuclease [Bacillus subtilis]   |

## S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop   | match<br>accession | match gene name  | % sim | % ident | length<br>(nt) |
|--------|-----|--------|--------|--------------------|--|-------|---------|----------------|
| ID     | ID  | (nt)   | (nt)   |                    |  |       |         |                |
| 517    | 2   | 1162   | 1614   | gi 166162          | Bacteriophage phi-11 int gene activator [Staphylococcus aceticiphage phi 11]   | 52    | 35      | 453            |
| 543    | 2   | 444    | 1295   | gi 1215693         | putative orf; GT9_orf434 [Mycoplasma pneumoniae]   | 52    | 25      | 852            |
| 586    | 1   | 1      | 336    | gi 581648          | epiB gene product [Staphylococcus epidermidis]   | 52    | 36      | 336            |
| 773    | 1   | 848    | 426    | gi 1279769         | FdhC [Methanobacterium thermoformicum]   | 52    | 30      | 423            |
| 1120   | 2   | 100    | 330    | gi 142439          | ATP-dependent nuclease [Bacillus subtilis]   | 52    | 35      | 231            |
| 1614   | 1   | 691    | 347    | gi 289262          | lcomE ORF3 [Bacillus subtilis]   | 52    | 28      | 345            |
| 2495   | 1   | 1      | 324    | gi 216151          | DNA polymerase (gene L; ttg start codon) [Bacteriophage SP02] gi 579197  | 52    | 34      | 324            |
|        |     |        |        |                    | SP02 DNA polymerase (aa 1-648) [Bacteriophage SP02] pir A21498 DJBPS2 DNA-<br>directed DNA polymerase (EC 2.7.7.7) - phage PC2 |       |         |                |
| 2931   | 1   | 566    | 285    | gi 1256136         | YbbG [Bacillus subtilis]   | 52    | 30      | 282            |
| 2943   | 1   | 577    | 320    | gi 41713           | lhisA ORF (AA 1-245) [Escherichia coli]  | 52    | 35      | 258            |
| 2993   | 1   | 588    | 295    | gi 298032          | EF [Streptococcus suis]  | 52    | 34      | 294            |
| 3667   | 1   | 612    | 307    | gi 849025          | hypothesitical 64.7-kDa protein [Bacillus subtilis]  | 52    | 36      | 306            |
| 3944   | 1   | 478    | 260    | gi 1218040         | IBAA [Bacillus licheniformis]  | 52    | 36      | 219            |
| 3954   | 2   | 613    | 347    | gi 854064          | U87 [Human herpesvirus 6]  | 52    | 50      | 267            |
| 3986   | 1   | 90     | 401    | gi 1205919         | Na <sup>+</sup> and Cl <sup>-</sup> dependent gamma-aminobutyric acid transporter [Haemophilus influenzae]                     | 52    | 33      | 312            |
| 4002   | 1   | 3      | 389    | gi 40003           | oxoglutarate dehydrogenase (NADP <sup>+</sup> ) [Bacillus subtilis] p P23129 CDO1_BACSU  | 52    | 42      | 387            |
|        |     |        |        |                    | 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (EC 2.4.2) (ALPHA- KETOGLU TARATE DEHYDROGENASE).                                    |       |         |                |
| 4020   | 1   | 1      | 249    | gi 159388          | ornithine decarboxylase [Leishmania donovani]  | 52    | 47      | 249            |
| 4098   | 1   | 438    | 220    | gi 409795          | No definition line found [Escherichia coli]  | 52    | 32      | 219            |
| 4248   | 1   | 3      | 212    | gi 965077          | Adr6p [Saccharomyces cerevisiae]   | 52    | 40      | 210            |
| 7      | 1   | 3      | 575    | gi 895747          | putative cel operon regulator [Bacillus subtilis]  | 51    | 28      | 573            |
| 21     | 4   | 2479   | 3276   | gi 1510962         | indole-3-glycerol phosphate synthase [Methanococcus jannaschii]  | 51    | 32      | 798            |
| 22     | 9   | 5301   | 5966   | gi 1303933         | YqiN [Bacillus subtilis]   | 51    | 25      | 666            |
| 43     | 3   | 1516   | 1283   | gi 1519460         | Srp1 [Schizosaccharomyces pombe]   | 51    | 31      | 234            |
| 44     | 117 | 111042 | 111305 | gi 42011           | lmoAD gene product [Escherichia coli]  | 51    | 35      | 264            |
| 51     | 111 | 6453   | 6731   | gi 495471          | vacuolating toxin [Helicobacter pylori]  | 51    | 37      | 279            |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF ID | Start (nt) | Stop (nt) | match accession | match gene name   | % sim | % ident | length (nt) |
|--------|--------|------------|-----------|-----------------|---|-------|---------|-------------|
| 52     | 4      | 2537       | 2995      | gi 12566552     | [25% identity to the E.coli regulatory protein MprA; putative [Bacillus subtilis]   | 51    | 32      | 459         |
| 57     | 10     | 7331       | 6843      | gi 508173       | [ELIA domain of PTS-dependent Gat transport and phosphorylation Escherichia coli]   | 51    | 32      | 489         |
| 59     | 1      | 29         | 1111      | gi 299163       | [alanine dehydrogenase [Bacillus subtilis]  | 51    | 33      | 1083        |
| 67     | 120    | 115791     | 116576    | gi 1510977      | [M. jannaschii predicted coding region MJ0938 [Methanococcus jannaschii]  | 51    | 24      | 786         |
| 69     | 2      | 1559       | 1218      | gi 467359       | [unknown [Bacillus subtilis]  | 51    | 34      | 342         |
| 71     | 1      | 3          | 1196      | gi 298032       | [EF [Streptococcus suis]  | 51    | 32      | 1194        |
| 78     | 1      | 349        | 176       | gi 1161242      | [proliferating cell nuclear antigen [Styela clava]  | 51    | 28      | 174         |
| 99     | 4      | 3357       | 4040      | gi 642795       | [TFIID subunit TAFI155 [Homo sapiens]   | 51    | 25      | 684         |
| 109    | 1      | 2852       | 1428      | gi 580920       | [rodd (gtaa) polypeptide (AA 1-673) [Bacillus subtilis] pir S06048 S06048<br>probable rodd protein - Bacillus subtilis sp(P13484)TAGE_BACSU PROBABLE<br>POLY(GLYCEROL-PHOSPHATE) LPHA-GLUCOSYLTRANSFERASE (EC 2.4.1.52) (TECHOIC<br>ACID BIOSYNTHESIS PROTEIN E). | 51    | 27      | 1425        |
| 109    | 9      | 6007       | 6693      | gi 1204815      | [hypothetical protein (SP:P32662) [Haemophilus influenzae]  | 51    | 23      | 687         |
| 112    | 3      | 1066       | 2352      | pir S05330 S053 | [maltose-binding protein precursor - Enterobacter aerogenes]  | 51    | 42      | 1287        |
| 112    | 113    | 14432      | 112855    | gi 405857       | [lyehU [Escherichia coli]   | 51    | 29      | 1578        |
| 114    | 9      | 9725       | 8967      | gi 435098       | [orf1 [Mycoplasma capricolum]   | 51    | 30      | 759         |
| 115    | 1      | 1          | 912       | gi 1431110      | [ORF YDL085w [Saccharomyces cerevisiae]   | 51    | 25      | 912         |
| 127    | 110    | 9647       | 110477    | gi 1204314      | [H. influenzae predicted coding region HI0056 [Haemophilus influenzae]  | 51    | 37      | 831         |
| 152    | 9      | 6814       | 7356      | gi 431929       | [MunI regulatory protein [Mycoplasma sp.]   | 51    | 38      | 543         |
| 154    | 2      | 575        | 1153      | gi 1237044      | [lunkown [Mycobacterium tuberculosis]   | 51    | 36      | 579         |
| 154    | 7      | 6587       | 5634      | gi 409286       | [lbumrU [Bacillus subtilis]   | 51    | 27      | 954         |
| 171    | 8      | 6943       | 6236      | gi 1205484      | [hypothetical protein (SP:P32918) [Haemophilus influenzae]  | 51    | 32      | 708         |
| 184    | 1      | 1          | 291       | gi 466886       | [B1496_C3_206 [Mycobacterium leprae]  | 51    | 33      | 291         |
| 212    | 5      | 1501       | 2139      | pir A45605 A456 | [mature-parasite-infected erythrocyte surface antigen MESA - Plasmodium<br>falciparum]  | 51    | 23      | 639         |
| 228    | 2      | 707        | 1378      | gi 8204         | [nuclear protein [Drosophila melanogaster]  | 51    | 27      | 672         |
| 236    | 8      | 8137       | 7481      | gi 49272        | [Asparaginase [Bacillus licheniformis]  | 51    | 31      | 657         |
| 243    | 4      | 4637       | 3546      | gi 1511102      | [Imelvalonate kinase [Methanococcus jannaschii]   | 51    | 29      | 1092        |

| Contig | ORF | Start | Stop | match           | gene name   | % sim | % ident | length |
|--------|-----|-------|------|-----------------|---|-------|---------|--------|
| ID     | ID  | (nt)  | (nt) | accession       |   | (nt)  | (nt)    |        |
| 257    | 4   | 3540  | 3373 | gi 1204579      | [H. influenzae predicted coding region H10326 [Haemophilus influenzae]        | 51    | 22      | 168    |
| 258    | 3   | 2397  | 1609 | gi 160299       | glutamic acid-rich protein [Plasmodium falciparum] pir A54514 A54514          | 51    | 34      | 789    |
|        |     |       |      |                 | glutamic acid-rich protein precursor - Plasmodium alciparum                   |       |         |        |
| 265    | 5   | 2419  | 3591 | gi 580841       | F1 [Bacillus subtilis]  | 51    | 32      | 1173   |
| 298    | 2   | 518   | 748  | gi 1336162      | SCP8 [streptococcus agalactiae]   | 51    | 34      | 231    |
| 316    | 9   | 5817  | 7049 | gi 413953       | ipa-29d gene product [Bacillus subtilis]                                      | 51    | 39      | 1233   |
| 332    | 2   | 3775  | 2057 | gi 1209012      | mutS [Thermus aquaticus thermophilus]   | 51    | 26      | 1719   |
| 364    | 4   | 3816  | 4991 | gi 528991       | unknown [Bacillus subtilis]   | 51    | 32      | 1176   |
| 440    | 2   | 448   | 684  | gi 2819         | transferase (GAL10) (AA 1 - 687) [Kluyveromyces lactis] pir S0107 XUVKG       | 51    | 32      | 237    |
|        |     |       |      |                 | UDPglucose 4-epimerase (EC 5.1.3.2) - yeast uyveromyces marxianus var. lactis |       |         |        |
| 495    | 2   | 1353  | 1177 | gi 297861       | protease G [Erwinia chrysanthemi]   | 51    | 41      | 177    |
| 495    | 3   | 2287  | 1718 | gi 1513317      | serine rich protein [Entamoeba histolytica]                                   | 51    | 25      | 570    |
| 506    | 1   | 840   | 421  | gi 455320       | CII protein [Bacteriophage P4]  | 51    | 33      | 420    |
| 600    | 1   | 1474  | 983  | gi 587532       | orf, len: 201, CAI: 0.16 [Saccharomyces cerevisiae] pir S48818 S48818         | 51    | 30      | 492    |
|        |     |       |      |                 | hypothetical protein - yeast (Saccharomyces cerevisiae)                       |       |         |        |
| 607    | 3   | 479   | 934  | gi 1511524      | hypothetical protein (SP:37002) [Methanococcus jannaschii]                    | 51    | 40      | 456    |
| 686    | 2   | 127   | 600  | gi 493017       | endocarditis specific antigen [Enterococcus faecalis]                         | 51    | 30      | 474    |
| 726    | 1   | 33    | 230  | gi 1353851      | unknown [Prochlorococcus marinus]   | 51    | 45      | 198    |
| 861    | 1   | 176   | 652  | gi 410145       | dehydroquinate dehydratase [Bacillus subtilis]                                | 51    | 34      | 477    |
| 869    | 1   | 782   | 393  | gi 40100        | rodC (tag3) polypeptide (AA 1-746) [Bacillus subtilis] pir S06049 S06049      | 51    | 23      | 390    |
|        |     |       |      |                 | rodC protein - Bacillus subtilis pir P13485 TAGF_BACSU_TECHOIC_ACID           |       |         |        |
|        |     |       |      |                 | BIOSYNTHESIS PROTEIN F.   |       |         |        |
| 1003   | 1   | 642   | 322  | gi 1279707      | hypothetical phosphoglycerate mutase [Saccharomyces cerevisiae]               | 51    | 39      | 321    |
| 1046   | 2   | 866   | 624  | gi 510257       | glycosyltransferase [Escherichia coli]  | 51    | 29      | 243    |
| 1467   | 1   | 702   | 352  | gi 1511175      | M. jannaschii predicted coding region MJ1177 [Methanococcus jannaschii]       | 51    | 32      | 351    |
| 2558   | 1   | 457   | 230  | isp P10582 IDPM | DNA POLYMERASE (EC 2.7.7.7) (S-1 DNA ORF 3).                                  | 51    | 26      | 228    |
| 3003   | 1   | 779   | 399  | gi 1809543      | CbrC protein [Erwinia chrysanthemi]   | 51    | 27      | 381    |
| 3604   | 1   | 1     | 1    | gi JC4210 JC42  | 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) - mouse                         | 51    | 37      | 399    |
| 3732   | 1   | 2     | 316  | gi 145906       | acyl-CoA synthetase [Escherichia coli]  | 51    | 33      | 315    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop   | match      | match gene name   |
|--------|-----|--------|--------|------------|---|
| ID     | ID  | (nt)   | (nt)   | accession  |   |
| 3791   | 1   | 1      | 2      | 274        | gi 1061351  semaphorin III family homolog [Homo sapiens]  |
| 3995   | 1   | 1      | 46     | 336        | gi 216346  surfactin synthetase [Bacillus subtilis]   |
| 4193   | 1   | 1      | 612    | 307        | gi 42749  ribosomal protein L12 (AA 1-179) [Escherichia coli] ir S04776 XXECPL   peptide N-acetyltransferase rnl (EC 2.3.1.-) - <i>cherichia coli</i> |
| 4539   | 1   | 1      | 367    | 185        | gi 1408494  homologous to penicillin acylase [Bacillus subtilis]  |
| 4562   | 1   | 1      | 442    | 239        | gi 1458280  coded for by <i>C. elegans</i> cDNA cm01e7; Similar to hydroxymethylglutaryl-CoA synthase [Caenorhabditis elegans]                        |
| 1      | 4   | 3576   | 4859   | gi 559160  | GRAIL score: null; cap site and late promoter motifs present pstream; putative [Autographa californica nuclear polyhedrosis virus]                    |
| 11     | 7   | 4044   | 5165   | gi 1146207 | putative [Bacillus subtilis]  |
| 11     | 13  | 110509 | 9496   | gi 1208451 | hypothetical protein [Synechocystis sp.]  |
| 19     | 1   | 2034   | 1018   | gi 1413966 | lipa-42d gene product [Bacillus subtilis]   |
| 20     | 11  | 8586   | 8407   | gi 1323159 | ORF YGR103w [Saccharomyces cerevisiae]  |
| 24     | 5   | 5408   | 4824   | gi 496280  | structural protein [Bacteriophage Tuc2009]  |
| 34     | 4   | 1926   | 2759   | gi 1303966 | YqjO [Bacillus subtilis]  |
| 38     | 30  | 122865 | 123440 | gi 1072179 | Similar to dihydroflavonol-4-reductase (maize, petunia, tomato)   [Caenorhabditis elegans]  |
| 47     | 2   | 1705   | 12976  | gi 153015  | FemA protein [Staphylococcus aureus]  |
| 56     | 13  | 115290 | 115841 | gi 606096  | ORF f167; end overlaps end of o100 by 14 bases; start overlaps f174, ther   starts possible [Escherichia coli]  |
| 57     | 1   | 2135   | 1077   | gi 640922  | xylitol dehydrogenase (unidentified hemiascomycete)   |
| 58     | 2   | 628    | 1761   | gi 143725  | putative [Bacillus subtilis]  |
| 88     | 6   | 4393   | 3884   | gi 1072179 | Similar to dihydroflavonol-4-reductase (maize, petunia, tomato)   [Caenorhabditis elegans]  |
| 89     | 5   | 3700   | 3356   | gi 1276658 | ORF174 gene product [Porphyra purpurea]   |
| 141    | 1   | 1      | 3      | 239        | gi 476024  carbamoyl phosphate synthetase II [Plasmidum falciparum]   |
| 151    | 1   | 1      | 186    | 626        | gi 1403441  unknown [Mycobacterium tuberculosis]  |
| 166    | 7   | 11065  | 9623   | gi 895747  | putative cel operon regulator [Bacillus subtilis]   |
| 201    | 6   | 5284   | 5096   | gi 1160229 | circumsporozoite protein [Plasmidum reichenowi]   |
| 206    | 122 | 130784 | 129555 | gi 1052754 | LmrP integral membrane protein [Lactococcus lactis]   |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop | match           | match gene name   | % sim | % ident | length |
|--------|-----|-------|------|-----------------|---|-------|---------|--------|
| ID     | ID  | (nt)  | (nt) | accession       |   | (nt)  |         | (nt)   |
| 211    | 4   | 1523  | 1927 | gi 410131       | ORF7 [Bacillus subtilis]  | 50    | 29      | 405    |
| 214    | 4   | 2411  | 3295 | sp P37348 YECE_ | HYPOTHETICAL PROTEIN IN ASPS 5' REGION (FRAGMENT).  | 50    | 37      | 885    |
| 228    | 7   | 5068  | 4406 | gi 313580       | envelope protein [Human immunodeficiency virus type 1] pir S35835 S35835  | 50    | 35      | 663    |
|        |     |       |      |                 | envelope protein - human immunodeficiency virus type 1 (fragment) [SUB 1-77]                                      |       |         |        |
| 272    | 2   | 3048  | 1723 | gi 1408485      | IB65G gene product [Bacillus subtilis]  | 50    | 22      | 1326   |
| 273    | 2   | 1616  | 984  | gi 984186       | phosphoglycerate mutase [Saccharomyces cerevisiae]  | 50    | 28      | 633    |
| 328    | 2   | 2507  | 1605 | gi 148896       | lipoprotein [Haemophilus influenzae]  | 50    | 26      | 903    |
| 332    | 4   | 5469  | 3802 | gi 1526547      | DNA polymerase family X [Thermus aquaticus]   | 50    | 27      | 1668   |
| 342    | 5   | 3473  | 3931 | gi 456562       | 6-box binding factor [Dictyostelium discoideum]   | 50    | 35      | 459    |
| 352    | 1   | 1478  | 741  | gi 288301       | ORF2 gene product [Bacillus megaterium]   | 50    | 29      | 738    |
| 408    | 7   | 5299  | 5523 | gi 11665        | ORF2136 [Marchantia polymorpha]   | 50    | 27      | 225    |
| 420    | 3   | 650   | 1825 | gi 757842       | UDP-sugar hydrolase [Escherichia coli]  | 50    | 30      | 1176   |
| 464    | 1   | 1     | 591  | gi 487282       | [Na+ -ATPase subunit J [Enterococcus hirae]   | 50    | 29      | 591    |
| 472    | 2   | 1418  | 864  | gi 551875       | BglR [Lactococcus lactis]   | 50    | 23      | 555    |
| 520    | 1   | 23    | 541  | gi 567036       | CapE [Staphylococcus aureus]  | 50    | 27      | 519    |
| 529    | 1   | 6     | 410  | gi 1256652      | 125% identity to the E.coli regulatory protein MrA; putative [Bacillus subtilis]                                  | 50    | 34      | 405    |
| 534    | 5   | 7726  | 6059 | gi 295671       | selected as a weak suppressor of a mutant of the subunit AC40 of DNA  | 50    | 18      | 1668   |
|        |     |       |      |                 | ependant RNA polymerase I and III [Saccharomyces cerevisiae]  |       |         |        |
| 647    | 1   | 2990  | 1497 | gi 405568       | [Tral protein shares sequence similarity with a family of oposomerases  | 50    | 31      | 1494   |
|        |     |       |      |                 | [Plasmid pSK41]   |       |         |        |
| 664    | 3   | 1133  | 711  | gi 410007       | leukocidin F component [Staphylococcus aureus, MRSA No. 4, Peptide, 23 aa]  | 50    | 32      | 423    |
| 678    | 1   | 1     | 627  | gi 298032       | [EF [Streptococcus suis]  | 50    | 29      | 627    |
| 755    | 3   | 947   | 1171 | gi 150572       | cytochrome c1 precursor (EC 1.10.2.2) [Paracoccus denitrificans] gi 45465   | 50    | 37      | 225    |
|        |     |       |      |                 | cytochrome c1 (AA 1-450) [Paracoccus denitrificans] pir C29413 C29413   |       |         |        |
|        |     |       |      |                 | ubiquinol-cytochrome-c reductase (EC 1.10.2.2) [cytochrome c1 precursor - Paracoccus denitrificans sp P13627 CY1] |       |         |        |
| 827    | 1   | 1363  | 683  | gi 142020       | heterocyst differentiation protein [Anabaena sp.]   | 50    | 21      | 681    |
| 892    | 1   | 3     | 752  | gi 1408485      | IB65G gene product [Bacillus subtilis]  | 50    | 27      | 750    |
| 910    | 2   | 438   | 887  | gi 1204727      | Tyrosine-specific transport protein [Haemophilus influenzae]  | 50    | 25      | 450    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop   | match            | gene name   | % sim | % ident | length |
|--------|-----|--------|--------|------------------|---|-------|---------|--------|
| ID     | ID  | (nt)   | (nt)   | accession        |   | (nt)  | (nt)    |        |
| 933    | 1   | 524    | 760    | lgi 1205451      | lcell division inhibitor [Haemophilus influenzae]                       | 50    | 32      | 237    |
| 973    | 1   | 424    | 236    | lgi 886947       | lorf3 gene product [Saccharomyces cerevisiae]                           | 50    | 40      | 189    |
| 1009   | 1   | 653    | 429    | lgi 153727       | lM protein [group G streptococcus]                                      | 50    | 28      | 225    |
| 1027   | 1   | 511    | 257    | lgi 413934       | lipa-10r gene product [Bacillus subtilis]                               | 50    | 25      | 255    |
| 1153   | 2   | 556    | 326    | lgi 773676       | lncCA [Alcaligenes xylosoxydans]  | 50    | 36      | 231    |
| 1222   | 1   | 798    | 400    | lgi 1408485      | lB65G gene product [Bacillus subtilis]                                  | 50    | 21      | 399    |
| 1350   | 1   | 692    | 399    | lgi 289272       | lferrichrome-binding protein [Bacillus subtilis]                        | 50    | 32      | 294    |
| 2945   | 1   | 366    | 184    | lgi 171704       | lhexasprenyl pyrophosphate synthetase (CQ01) [Saccharomyces cerevisiae] | 50    | 34      | 183    |
| 2968   | 2   | 1604   | 804    | lgi 397526       | lclumping factor [Staphylococcus aureus]                                | 50    | 33      | 801    |
| 2998   | 2   | 657    | 394    | lgi 495696       | lF54E7_3 gene product [Caenorhabditis elegans]                          | 50    | 40      | 264    |
| 3046   | 2   | 506    | 306    | lpir S13819 S138 | lacyl carrier protein - Anabaena variabilis (fragment)                  | 50    | 32      | 201    |
| 3063   | 1   | 547    | 275    | lgi 474190       | liuA gene product [Escherichia coli]                                    | 50    | 29      | 273    |
| 3174   | 1   | 3      | 146    | lgi 151900       | lalcohol dehydrogenase [Rhodobacter sphaeroides]                        | 50    | 31      | 144    |
| 3792   | 1   | 625    | 314    | lgi 1001423      | lhypothetical protein [Synochocystis sp.]                               | 50    | 35      | 312    |
| 3800   | 1   | 2      | 262    | lgi 144733       | [NAD-dependent beta-hydroxybutyryl coenzyme A dehydrogenase Clostridium | 50    | 28      | 261    |
|        |     |        |        |                  | lacetobutylicum]  |       |         |        |
| 3946   | 1   | 373    | 188    | lgi 576765       | lcytochrome b [Myrmecia pilosula]                                       | 50    | 38      | 186    |
| 3984   | 1   | 578    | 291    | lsp P37348 YECE_ | lHYPOTHETICAL PROTEIN IN ASPS 5' REGION (FRAGMENT).                     | 50    | 37      | 288    |
| 37     | 110 | 8250   | 7885   | lgi 1204367      | lhypothetical protein (GB:U14003_278) [Haemophilus influenzae]          | 49    | 30      | 366    |
| 46     | 116 | 113802 | 114848 | lgi 4668860      | lacd; B1308_F1_34 [Mycobacterium leprae]                                | 49    | 24      | 1047   |
| 59     | 5   | 2267   | 3601   | lgi 1606304      | lORF_0462 [Escherichia coli]  | 49    | 27      | 1335   |
| 112    | 118 | 117884 | 118615 | lgi 559502       | lND4 protein (AA 1 - 409) [Caenorhabditis elegans]                      | 49    | 25      | 732    |
| 138    | 9   | 6973   | 7902   | lgi 303953       | lesterase [Acinetobacter calcoaceticus]                                 | 49    | 29      | 930    |
| 217    | 6   | 4401   | 5138   | lgi 496254       | lfibronectin/fibrinogen-binding protein [Streptococcus pyogenes]        | 49    | 31      | 738    |
| 220    | 112 | 111803 | 112657 | lgi 397526       | lclumping factor [Staphylococcus aureus]                                | 49    | 31      | 855    |
| 228    | 4   | 1842   | 2492   | lpir S23692 S236 | lhypothetical protein 9 - Plasmodium falciparum                         | 49    | 24      | 651    |
| 268    | 1   | 5016   | 2614   | lgi 143047       | lORFB [Bacillus subtilis]   | 49    | 26      | 2403   |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop  | match           | match gene name  |
|--------|-----|-------|-------|-----------------|--|
| ID     | ID  | (nt)  | (nt)  | accession       | (nt)   |
| 271    | 2   | 1164  | 1373  | gi 11001257     | hypothesetical protein [Synechocystis sp.]   |
| 300    | 3   | 4340  | 3180  | gi 1510796      | hypothesetical protein (GP:X91006_2) [Methanococcus jannaschii]  |
| 381    | 1   | 2281  | 1142  | gi 396301       | matches PS00041: Bacterial regulatory proteins, arac family signature<br>[Escherichia coli]  |
| 466    | 1   | 3     | 947   | gi 1303863      | Yqgp [Bacillus subtilis]   |
| 666    | 1   | 379   | 191   | gi 633112       | ORF1 [Streptococcus sobrinus]  |
| 670    | 2   | 403   | 1014  | gi 1122758      | lunknow [Bacillus subtilis]  |
| 709    | 1   | 1433  | 795   | gi 143830       | lxpac [Bacillus subtilis]  |
| 831    | 1   | 943   | 473   | gi 401786       | phosphomannomutase [Mycoplasma pirum]  |
| 1052   | 1   | 422   | 213   | gi 1303799      | YqeN [Bacillus subtilis]   |
| 1800   | 1   | 342   | 172   | gi 216300       | peptidoglycan synthesis enzyme [Bacillus subtilis] sp P37585 MURG_BACSU<br>MURG PROTEIN UDP-N-ACETYLGLUCOSAMINE-N-ACETYLUMURAMYLPENTAPEPTIDE) PYROPHORYL-UNDECAPRENOL N-ACETYLGLUCOSAMINE TRANSFERASE. |
| 2430   | 1   | 2     | 376   | sp P27434 YFGA_ | HYPOTHETICAL 36.2 KD PROTEIN IN NDK-GCP1 INTERGENIC REGION.  |
| 3096   | 1   | 542   | 273   | gi 516360       | surfactin synthetase [Bacillus subtilis]   |
| 32     | 4   | 3771  | 3100  | gi 1217963      | hepatocyte nuclear factor 4 gamma (HNF4gamma) [Homo sapiens]   |
| 38     | 1   | 1     | 609   | gi 1205790      | [H. influenzae predicted coding region HI11555 [Haemophilus influenzae]  |
| 45     | 6   | 5021  | 6427  | gi 1524267      | unknown [Mycobacterium tuberculosis]   |
| 59     | 14  | 16346 | 31096 | gi 1197336      | Lmp3 protein [Mycoplasma hominis]  |
| 61     | 1   | 3     | 608   | gi 1511555      | quinolone resistance norA protein [Methanococcus jannaschii]   |
| 61     | 3   | 3311  | 3646  | gi 1303893      | Yqhl [Bacillus subtilis]   |
| 114    | 1   | 98    | 415   | gi 671708       | (su(s)) homolog; similar to Drosophila melanogaster suppressor of able (su(s)) protein, Swiss-Prot Accession Number P22293 Drosophila virilis]   |
| 121    | 1   | 1131  | 610   | gi 1314584      | lunknow [Sphingomonas S88]   |
| 136    | 1   | 2014  | 1280  | gi 1205968      | [H. influenzae predicted coding region HI11738 [Haemophilus influenzae]  |
| 171    | 10  | 8220  | 9557  | gi 1208454      | hypothesetical protein [Synechocystis sp.]   |
| 175    | 1   | 3625  | 1814  | gi 396400       | similar to eukaryotic Na <sup>+</sup> /H <sup>+</sup> exchangers [Escherichia coli]<br>sp P32703 YJCE_ECOLI HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS NTERGENIC REGION (O549).                          |
| 194    | 1   | 2     | 385   | gi 1510493      | M. jannaschii predicted coding region MJ0419 [Methanococcus jannaschii]  |

## S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop   | match           | match gene name   | % sim  | % ident | length |      |
|--------|-----|-------|--------|-----------------|---|--|---------|--------|------|
| ID     | ID  | (nt)  | (nt)   | accession       |   |  |         | (nt)   |      |
| 197    | 1   | 1     | 901    | 452             | gi 1045714  | Spermidine/putrescine transport ATP-binding protein [Mycoplasma genitalium]  | 48      | 25     | 450  |
| 203    | 1   | 1     | 1      | 396             | gi 940288   | protein localized in the nucleoli of pea nuclei; ORF; putative Pisum sativum | 48      | 29     | 396  |
| 204    | 1   | 1     | 1363   | 698             | gi 529202   | !No definition line found [Caenorhabditis elegans]                           | 48      | 25     | 666  |
| 206    | 120 | 34815 | 127760 | gi 511490       | Igramicidin S synthetase 2 [Bacillus brevis]                          | 48   | 27      | 7056   |      |
| 212    | 1   | 1     | 2      | 166             | gi 295899   | Inucleolin [Xenopus laevis]  | 48      | 34     | 165  |
| 220    | 110 | 12652 | 11426  | gi 44073        | ISecY protein [Lactococcus lactis]                                    | 48   | 23      | 1227   |      |
| 243    | 1   | 6     | 6450   | 5491            | gi 1184118  | lmevalonate kinase [Methanobacterium thermoautotrophicum]                    | 48      | 30     | 960  |
| 264    | 4   | 5434  | 3308   | gi 1015903      | !ORF YUR151c [Saccharomyces cerevisiae]                               | 48   | 26      | 2127   |      |
| 441    | 1   | 1     | 1532   | 768             | gi 142863   | replication initiation protein [Bacillus subtilis] pir B26580                | 48      | 23     | 765  |
| 444    | 5   | 3898  | 5298   | gi 145836       | !replication initiation protein - Bacillus subtilis                   | 48   | 24      | 1401   |      |
| 484    | 1   | 2     | 388    | 1110            | gi 146551   | !transmembrane protein (kdpD) [Escherichia coli]                             | 48      | 18     | 723  |
| 542    | 3   | 1425  | 2000   | pir S28969 S289 | IN-carbamoylsarcosine amidohydrolase (EC 3.5.1.59) - Arthrobacter sp. | 48   | 27      | 576    |      |
| 566    | 1   | 1     | 3      | 1019            | gi 153490   | !tetracycline C resistance and export protein [Streptomyces laucessens]      | 48      | 24     | 1017 |
| 611    | 1   | 1     | 2      | 730             | gi 1103507  | !unknown [Schizosaccharomyces pombe]   | 48      | 38     | 729  |
| 624    | 1   | 1     | 1255   | 665             | gi 144859   | !ORF B [Clostridium perfringens]   | 48      | 26     | 591  |
| 846    | 1   | 1     | 1014   | 508             | gi 537506   | !paramyosin [Dirofilaria immitis]  | 48      | 27     | 507  |
| 1020   | 1   | 1     | 66     | 950             | gi 1499876  | !magnesium and cobalt transport protein [Methanococcus jannaschii]           | 48      | 30     | 885  |
| 1227   | 1   | 1     | 1      | 174             | gi 493730   | !lipoxigenase [Pisum sativum]  | 48      | 35     | 174  |
| 1266   | 1   | 1     | 1      | 405             | gi 882452   | !ORF f211; alternate name yggA; orf5 of X14436 (Escherichia coli) gi 41425   | 48      | 24     | 405  |
| 2071   | 1   | 1     | 707    | 381             | gi 1408486  | !HS74A gene product [Bacillus subtilis]                                      | 48      | 25     | 327  |
| 2398   | 1   | 1     | 463    | 233             | gi 1500401  | !reverse gyrase [Methanococcus jannaschii]                                   | 48      | 40     | 231  |
| 2425   | 1   | 1     | 476    | 246             | pir H48563 H485   | !G1 protein - fowlpox virus (strain HP444) (fragment)                        | 48      | 40     | 231  |
| 2432   | 1   | 1     | 446    | 225             | gi 1353703  | !Trio [Homo sapiens]   | 48      | 33     | 222  |
| 2453   | 1   | 1     | 794    | 399             | gi 1142850  | !division initiation protein [Bacillus subtilis]                             | 48      | 29     | 396  |
| 2998   | 1   | 1     | 469    | 236             | gi 577569   | !PepV [Lactobacillus delbrueckii]  | 48      | 31     | 234  |

## S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop   | match            | match gene name   | % sim | % ident | length |
|--------|-----|-------|--------|------------------|---|-------|---------|--------|
| ID     | ID  | (nt)  | (nt)   | accession        |   |       |         | (nt)   |
| 3042   | 1   | 14    | 1280   | gi 945219        | Imucin [Homo sapiens]   | 48    | 35      | 267    |
| 3686   | 1   | 1     | 405    | gi 145836        | Putative [Escherichia coli]   | 48    | 25      | 405    |
| 4027   | 2   | 492   | 301    | lpir S51177 S511 | trans-activator protein - Equine infectious anemia virus  | 48    | 32      | 192    |
| 4      | 2   | 3641  | 2232   | gi 1303989       | IYqkI [Bacillus subtilis]   | 47    | 24      | 1410   |
| 24     | 2   | 599   | 1084   | gi 540083        | IPCA-1 gene product [Bradysia hygida]   | 47    | 28      | 486    |
| 36     | 110 | 7524  | 6925   | gi 1209223       | Lesterase [Acinetobacter lwoffii]   | 47    | 26      | 600    |
| 43     | 2   | 196   | 1884   | gi 1403455       | Unknown [Mycobacterium tuberculosis]  | 47    | 27      | 1689   |
| 44     | 122 | 16118 | 115108 | gi 1511555       | Quinolone resistance norA protein [Methanococcus jannaschii]  | 47    | 31      | 1011   |
| 69     | 7   | 7141  | 6710   | gi 438466        | Possible operon with orfG. Hydrophilic, no homologue in the database; putative [Bacillus subtilis]  | 47    | 29      | 432    |
| 81     | 4   | 5022  | 4279   | gi 466882        | lpps1; B1496_C2_189 [Mycobacterium leprae]  | 47    | 24      | 744    |
| 120    | 12  | 9135  | 8863   | gi 927340        | D9509_27p; CAI: 0.12 [Saccharomyces cerevisiae]   | 47    | 38      | 273    |
| 142    | 1   | 2022  | 1174   | gi 486143        | lORF YKL094w [Saccharomyces cerevisiae]   | 47    | 32      | 849    |
| 168    | 1   | 2178  | 1093   | gi 1177254       | Hypothetical EcsB protein [Bacillus subtilis]   | 47    | 29      | 1086   |
| 263    | 1   | 1884  | 943    | gi 142822        | D-alanine racemase cds [Bacillus subtilis]  | 47    | 34      | 942    |
| 279    | 1   | 1109  | 561    | gi 516608        | 12 predicted membrane helices, homology with B. subtilis men Orf3 Rowland et. al. unpublished Accession number M74183), approximately 1 minutes on updated Rudd map; putative [Escherichia coli] sp P37355 YFBB_ECOLI | 47    | 31      | 549    |
| 345    | 2   | 2620  | 1676   | gi 1204835       | Hippuricase [Haemophilus influenzae]  | 47    | 28      | 945    |
| 389    | 2   | 152   | 400    | gi 456562        | IG-box binding factor [Dictyostelium discoideum]  | 47    | 32      | 249    |
| 391    | 1   | 1     | 831    | gi 1420856       | Imyo-inositol transporter [Schizosaccharomyces pombe]   | 47    | 19      | 831    |
| 404    | 3   | 2072  | 2773   | gi 1255425       | IC33G8_2 gene product [Caenorhabditis elegans]  | 47    | 17      | 702    |
| 529    | 5   | 2145  | 3107   | gi 1303973       | IYqjV [Bacillus subtilis]   | 47    | 29      | 963    |
| 565    | 2   | 2321  | 1257   | gi 142824        | Processing protease [Bacillus subtilis]   | 47    | 28      | 1065   |
| 654    | 1   | 962   | 483    | gi 243353        | lORF 5' of ECRF3 [herpesvirus saimiri HVS, host-squirrel monkey, peptide, 407 aa]   | 47    | 23      | 480    |
| 692    | 1   | 115   | 633    | gi 150756        | 140 kDa protein [Plasmid pJM1]  | 47    | 25      | 519    |
| 765    | 1   | 1634  | 819    | gi 1256621       | 126.7% of identity in 165 aa to a Thermophilic bacterium hypothetical protein 6; putative [Bacillus subtilis]   | 47    | 28      | 816    |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | lORE | Start | Stop  | match         | match gene name   | % sim | % ident | length |
|--------|------|-------|-------|---------------|---|-------|---------|--------|
| ID     | ID   | (nt)  | (nt)  | accession     |   | (nt)  | (nt)    |        |
| 825    | 1    | 211   | 1023  | gi 397526     | clumping factor [Staphylococcus aureus]   | 1     | 47      | 32     |
| 914    | 1    | 1     | 615   | gi 558073     | polymorphic antigen [Plasmodium falciparum]   | 1     | 47      | 29     |
| 1076   | 1    | 1     | 753   | gi 1147557    | Aspartate aminotransferase [Bacillus circulans]   | 1     | 47      | 33     |
| 1351   | 1    | 793   | 398   | gi 755153     | ATP-binding protein [Bacillus subtilis]   | 1     | 47      | 20     |
| 4192   | 1    | 1     | 3     | gi 145836     | putative [Escherichia coli]   | 1     | 47      | 24     |
| 5      | 6    | 4708  | 4361  | gi 305080     | myosin heavy chain [Entamoeba histolytica]  | 1     | 46      | 30     |
| 11     | 4    | 2777  | 3058  | gi 603639     | Yel040p [Saccharomyces cerevisiae]  | 1     | 46      | 28     |
| 46     | 11   | 10518 | 10300 | gi 1246901    | ATP-dependent DNA ligase [Candida albicans]   | 1     | 46      | 28     |
| 61     | 4    | 3941  | 7930  | gi 298032     | EF [Streptococcus suis]   | 1     | 46      | 35     |
| 132    | 4    | 5028  | 4093  | gi 1511057    | hypothesitical protein SP:PI5869 [Methanococcus jannaschii]   | 1     | 46      | 25     |
| 170    | 4    | 4719  | 3652  | gi 5191015519 | IG4 protein - Sauroleishmania tarentolae  | 1     | 46      | 26     |
| 191    | 7    | 9543  | 8284  | gi 1041334    | lF54D5.7 [Caenorhabditis elegans]   | 1     | 46      | 25     |
| 253    | 1    | 1     | 396   | gi 1204449    | dihydroliopamide acetyltransferase [Haemophilus influenzae]   | 1     | 46      | 35     |
| 264    | 3    | 437   | 973   | gi 180189     | l cerebellar-degeneration-related antigen (CDR34) [Homo sapiens] gi 1182737   | 1     | 46      | 29     |
| 384    | 1    | 1     | 2     | 862           | gi 1221884 (urea?) amidolyase [Haemophilus influenzae] cerebellar degeneration-associated protein [Homo sapiens] gi A29770 A29770 cerebellar degeneration-related protein - human | 1     | 46      | 31     |
| 273    | 1    | 485   | 285   | gi 607573     | envelope glycoprotein C2V3 region [Human immunodeficiency virus type ]  | 1     | 46      | 35     |
| 350    | 1    | 1     | 3     | 563           | gi 537052 ORF f286 [Escherichia coli]   | 1     | 46      | 35     |
| 384    | 1    | 1     | 2     | 862           | gi 1221884 (urea?) amidolyase [Haemophilus influenzae] cerebellar degeneration-associated protein [Homo sapiens] gi A29770 A29770 cerebellar degeneration-related protein - human | 1     | 46      | 31     |
| 410    | 4    | 1876  | 2490  | gi 1110518    | proton antiporter efflux pump [Mycobacterium smegmatis]   | 1     | 46      | 24     |
| 432    | 1    | 2663  | 1455  | gi 1197634    | orf4; putative transporter; Method: conceptual translation supplied by author [Mycobacterium smegmatis]   | 1     | 46      | 27     |
| 458    | 1    | 2419  | 1211  | gi 15470      | lportal protein [Bacteriophage SPP1]  | 1     | 46      | 30     |
| 517    | 5    | 2477  | 4192  | gi 1523812    | lorf5 [Bacteriophage A2]  | 1     | 46      | 23     |
| 540    | 3    | 1512  | 1285  | gi 215635     | lpacA [Bacteriophage P1]  | 1     | 46      | 30     |
| 587    | 2    | 649   | 1242  | gi 537148     | lORF f181 [Escherichia coli]  | 1     | 46      | 29     |
| 1218   | 1    | 747   | 391   | gi 1205456    | l single-stranded-DNA-specific exonuclease [Haemophilus influenzae]   | 1     | 46      | 30     |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start  | Stop   | match<br>accession | match gene name  | % sim | % ident | length<br>(nt) |
|--------|-----|--------|--------|--------------------|--|-------|---------|----------------|
| ID     | ID  | (nt)   | (nt)   |                    |  |       |         |                |
| 3685   | 1   | 1      | 402    | gi 450688          | hsdM gene of EcoprrI gene product [Escherichia coli] pir S38437 S38437 hsdM              | 46    | 33      | 402            |
|        |     |        |        |                    | protein - Escherichia coli pir S09629 S09629 hypothetical protein A -                    |       |         |                |
|        |     |        |        |                    | Escherichia coli (SUB 40-520)  |       |         |                |
| 4176   | 1   | 673    | 338    | gi 951460          | FIM-C.1 gene product [Xenopus laevis]  | 46    | 31      | 336            |
| 37     | 7   | 4813   | 5922   | gi 606064          | ORF f408 [Escherichia coli]  | 45    | 24      | 1110           |
| 38     | 116 | 111699 | 112004 | gi 452192          | protein tyrosine phosphatase (PTP-BAS, type 2) [Homo sapiens]                            | 45    | 24      | 306            |
| 87     | 2   | 1748   | 2407   | gi 1061813         | homologous to sp:PHOR_BACSU [Bacillus subtilis]  | 45    | 23      | 660            |
| 103    | 112 | 141482 | 113385 | gi 1001307         | hypothetical protein [Synechocystis sp.]   | 45    | 22      | 798            |
| 112    | 14  | 114791 | 113811 | gi 1204389         | H. influenzae predicted coding region HI0131 [Haemophilus influenzae]                    | 45    | 23      | 981            |
| 145    | 4   | 4483   | 3461   | gi 220578          | open reading frame [Mus musculus]  | 45    | 20      | 1023           |
| 170    | 6   | 6329   | 4965   | gi 238657          | AppC-cytochrome d oxidase, subunit I homolog [Escherichia coli, K12,<br>epitope, 514 aa] | 45    | 27      | 1365           |
| 206    | 2   | 5230   | 4346   | gi 1222056         | aminotransferase [Haemophilus influenzae]  | 45    | 27      | 885            |
| 228    | 1   | 60     | 716    | gi 1160299         | glutamic acid-rich protein [Plasmodium falciparum] pir A54514 A54514                     | 45    | 23      | 657            |
|        |     |        |        |                    | glutamic acid-rich protein precursor - Plasmodium alciparum                              |       |         |                |
| 288    | 1   | 1      | 2      | gi 1015            | C33G8.2 gene product [Caenorhabditis elegans]  | 45    | 23      | 1014           |
| 313    | 3   | 4339   | 3128   | gi 581140          | NADH dehydrogenase [Escherichia coli]  | 45    | 30      | 1212           |
| 332    | 1   | 1      | 914    | gi 459             | F47A4.2 [Caenorhabditis elegans]   | 45    | 20      | 456            |
| 344    | 1   | 1      | 3      | gi 171225          | kinesin-related protein [Saccharomyces cerevisiae]                                       | 45    | 26      | 219            |
| 441    | 2   | 1      | 1501   | gi 1073            | replication initiation protein [Bacillus subtilis] pir B26580 B26580                     | 45    | 27      | 429            |
|        |     |        |        |                    | replication initiation protein - Bacillus subtilis                                       |       |         |                |
| 672    | 1   | 1      | 2      | gi 1511334         | M. jannaschii predicted coding region MJ1323 [Methanococcus jannaschii]                  | 45    | 22      | 981            |
| 763    | 3   | 1345   | 851    | gi 606180          | ORF f310 [Escherichia coli]  | 45    | 24      | 495            |
| 886    | 3   | 379    | 846    | gi 726426          | similar to protein kinases and C. elegans proteins F37C12.8 and 37C12.5                  | 45    | 30      | 468            |
|        |     |        |        |                    | [Caenorhabditis elegans]   |       |         |                |
| 948    | 1   | 1      | 3      | gi 156400          | myosin heavy chain (isozyme unc-54) [Caenorhabditis elegans]                             | 45    | 25      | 471            |
|        |     |        |        |                    | pir A93958 MKW myosin heavy chain B - Caenorhabditis elegans                             |       |         |                |
|        |     |        |        |                    | sp P02366 MYSB_CAEEL MYOSIN HEAVY CHAIN B (MHC B).                                       |       |         |                |
| 1158   | 1   | 1      | 2      | gi 441155          | transmission-blocking target antigen [Plasmodium falciparum]                             | 45    | 35      | 375            |
| 2551   | 1   | 1      | 4      | gi 1276705         | ORF287 gene product [Porphyra purpurea]  | 45    | 28      | 282            |
| 3967   | 1   | 1      | 42     | gi 976025          | HRSA [Escherichia coli]  | 45    | 28      | 333            |

| Contig | ORF | Start  | Stop   | match            | match gene name   | % sim | % ident | length |
|--------|-----|--------|--------|------------------|---|-------|---------|--------|
| ID     | ID  | (nt)   | (nt)   | accession        |   | (nt)  | (nt)    |        |
| 52     | 7   | 6931   | 5846   | gi 467378        | unknown [Bacillus subtilis]   | 44    | 22      | 1086   |
| 138    | 8   | 6475   | 6849   | gi 173028        | lthioredoxin II [Saccharomyces cerevisiae]  | 44    | 28      | 375    |
| 221    | 5   | 7032   | 5617   | gi 153490        | tetracenomycin C resistance and export protein [Streptomyces laucaescens]   | 44    | 21      | 1416   |
| 252    | 2   | 1331   | 1122   | gi 1204989       | hypothesitical protein (GB:U00022_9) [Haemophilus influenzae]   | 44    | 30      | 210    |
| 263    | 2   | 3265   | 2093   | gi 1136221       | carboxypeptidase [Sulfolobus solfataricus]  | 44    | 26      | 1173   |
| 365    | 4   | 4963   | 3524   | gi 1296822       | orf1 gene product [Lactobacillus helveticus]  | 44    | 31      | 1440   |
| 543    | 3   | 1315   | 1833   | gi 1063250       | low homology to P20 protein of Bacillus licheniformis and bleomycin acetyltransferase of Streptomyces verticillus [Bacillus subtilis] | 44    | 24      | 519    |
| 544    | 4   | 3942   | 4892   | gi 951460        | FIM-C.1 gene product [Xenopus laevis]   | 44    | 32      | 951    |
| 792    | 1   | 1224   | 613    | gi 205680        | high molecular weight neurofilament [Rattus norvegicus]   | 44    | 28      | 612    |
| 44     | 18  | 11303  | 11911  | gi 1511614       | l-molybdopterin-quanine dinucleotide biosynthesis protein A [Methanococcus jannaschii]  | 43    | 27      | 609    |
| 59     | 8   | 3665   | 5128   | gi 153490        | tetracenomycin C resistance and export protein [Streptomyces laucaescens]   | 43    | 21      | 1464   |
| 59     | 10  | 5536   | 7527   | gi 153022        | lipase [Staphylococcus epidermidis]   | 43    | 22      | 1992   |
| 99     | 1   | 1346   | 681    | gi 1419051       | unknown [Mycobacterium tuberculosis]  | 43    | 21      | 666    |
| 310    | 8   | 9402   | 112134 | gi 397526        | clumping factor [Staphylococcus aureus]   | 43    | 21      | 2733   |
| 432    | 3   | 2782   | 2303   | pir A6050 A605   | sporozoite surface protein 2 - Plasmodium yoelii (fragment)   | 43    | 29      | 480    |
| 519    | 3   | 2547   | 3122   | sp Q06530 DHSU_- | SULFIDE DEHYDROGENASE (FLAVOCYTOCHROME C) FLAVOPROTEIN CHAIN PRECURSOR (EC 1.8.2.-) (FCSD).   | 43    | 23      | 576    |
| 4      | 113 | 112053 | 13321  | gi 295671        | selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependent RNA polymerase I and III [Saccharomyces cerevisiae]    | 42    | 18      | 1269   |
| 94     | 2   | 1768   | 1091   | gi 501027        | ORF2 [Trypanosoma brucei]   | 42    | 31      | 678    |
| 127    | 4   | 5791   | 4550   | gi 42029         | ORF1 gene product [Escherichia coli]  | 42    | 21      | 1242   |
| 297    | 3   | 1515   | 1036   | gi 142790        | ORF1; putative [Bacillus firmus]  | 42    | 25      | 480    |
| 344    | 6   | 4097   | 3525   | gi 40320         | ORF 2 (AA 1-203) [Bacillus thuringiensis]   | 42    | 30      | 573    |
| 512    | 1   | 2167   | 1115   | gi 405957        | lyeeF [Escherichia coli]  | 42    | 23      | 1053   |
| 631    | 1   | 2434   | 1223   | gi 580920        | rodd (grtA) polypeptide (AA 1-673) [Bacillus subtilis] Pir S06048 S06048  | 42    | 24      | 1212   |
|        |     |        |        |                  | probable rodd protein - Bacillus subtilis sp P13484 TAGE_BACSU PROBABLE   |       |         |        |
|        |     |        |        |                  | POLY(GLYCEROL-PHOSPHATE) LPHA-GLUCOSYLTRANSFERASE (EC 2.4.1.52) (TECHOIC ACID BIOSYNTHESIS PROTEIN E)                                 |       |         |        |

S. aureus - Putative coding regions of novel proteins similar to known proteins

| Contig | ORF | Start | Stop  | match           | match gene name  | % sim | % ident | length |
|--------|-----|-------|-------|-----------------|--|-------|---------|--------|
| ID     | ID  | (nt)  | (nt)  | accession       |  | (nt)  |         | (nt)   |
| 685    | 3   | 2359  | 1739  | gi 1303784      | YqeD [Bacillus subtilis]   | 42    | 19      | 621    |
| 4132   | 1   | 787   | 395   | gi 1022910      | protein tyrosine phosphatase [Dictyostelium discoideum]  | 42    | 25      | 393    |
| 86     | 2   | 1375  | 884   | gi 309506       | spermidine/spermine N1-acetyltransferase [Mus saxicola] pir S43430 S43430  | 41    | 30      | 492    |
| 191    | 12  | 14797 | 14075 | gi 1124957      | lorf4 gene product [Methanoscarcina barkeri]   | 41    | 22      | 723    |
| 212    | 6   | 2150  | 3127  | gi 15873        | observed 35.2kD protein [Mycobacteriophage 15]   | 41    | 26      | 978    |
| 213    | 3   | 1263  | 2000  | gi 633692       | TrsA [Yersinia enterocolitica]   | 41    | 18      | 738    |
| 408    | 4   | 2625  | 3386  | gi 1197634      | lorf4; putative transporter; Method: conceptual translation supplied by author [Mycobacterium smegmatis]   | 41    | 24      | 762    |
| 542    | 1   | 3     | 1103  | gi 457146       | rhoptry protein [Plasmodium yoelii]  | 41    | 21      | 1101   |
| 924    | 1   | 2     | 475   | pir JH0148 JH01 | nucleolin - rat  | 41    | 30      | 474    |
| 1562   | 1   | 1     | 402   | gi 552184       | asparagine-rich antigen Pfa35-2 [Plasmodium falciparum] pir S27826 S27826  | 40    | 20      | 402    |
| 2395   | 1   | 518   | 261   | pir S42251 S422 | hypothetical protein 5 - fowlpox virus   | 40    | 18      | 258    |
| 4077   | 1   | 3     | 305   | gi 1055055      | I coded for by C. elegans cDNA yk37g1.5; coded for by C. elegans cDNA yk5c9.5; coded for by C. elegans cDNA yk1g9.5; alternatively spliced form of F52C9.8b [Caenorhabditis elegans] | 39    | 21      | 303    |
| 958    | 1   | 1003  | 503   | gi 1255425      | IC33G8.2 gene product [Caenorhabditis elegans]   | 37    | 25      | 501    |
| 59     | 12  | 8294  | 10636 | gi 535260       | ISTARP antigen [Plasmodium reichenowi]   | 36    | 24      | 2343   |
| 63     | 5   | 3550  | 8079  | gi 298032       | EF [Streptococcus suis]  | 36    | 19      | 4530   |
| 544    | 3   | 2507  | 3601  | gi 1015903      | ORF YUR15IC [Saccharomyces cerevisiae]   | 35    | 22      | 1095   |
| 63     | 4   | 1949  | 3574  | gi 552195       | circumsporozoite protein [Plasmodium falciparum] sp P05691 CSP_PLAFL   | 32    | 27      | 1626   |
|        |     |       |       |                 | CIRCUIMSPOROZOITE PROTEIN (CS) (FRAGMENT)  |       |         |        |